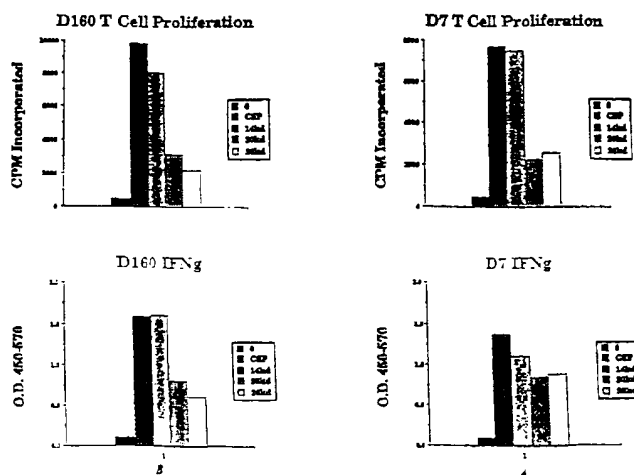




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(71) Applicant: CORIXA CORPORATION [US/US]; 1124 Columbia Street, Seattle, WA 98104 (US).		<p>Published</p> <p><i>With declaration under Article 17(2)(a); without abstract; title not checked by the International Searching Authority.</i></p>	
(72) Inventors: REED, Steven, G.; 2843 122nd Place N.E., Bellevue, WA 98005 (US). SKEIKY, Yasir, A., W.; 8327 25th Street, Seattle, WA 98107 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). CAMPOS-NETO, Antonio; 9308 Midship Court N.E., Bainbridge Island, WA 98110 (US). HOUGHTON, Raymond; 2636 242nd Place S.E., Bothell, WA 98021 (US). VEDVICK, Thomas, S.; 124 South 300th Place, Federal Way, WA 98003 (US). TWARDZIK, Daniel, R.; 10195 South Beach Drive, Bainbridge Island, WA 98110 (US). LODES, Michael, J.; 9223 36th Avenue S.W., Seattle, WA 98126 (US). HENDRICKSON, Ronald, C.; 4114 S.W. Charlestown Street, Seattle, WA 98116 (US).			

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COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Application
5 No. 09/024,753, filed February 18, 1998; which is a continuation-in-part of
U.S. Application No. 08/942,341, filed October 1, 1997; which is a continuation-in-part
of U.S. Application No. 08/818,111, filed March 13, 1997, which is a continuation-in-
part of U.S. Application No. 08/729,622 filed October 11, 1996; which claims priority
from PCT Application No. PCT/US 96/14675, filed August 30, 1996; and is a
10 continuation-in-part of U.S. Application No. 08/680,574, filed July 12, 1996; which is a
continuation-in-part of U.S. Application No. 08/658,800 filed June 5, 1996; which is a
continuation-in-part of U.S. Application No. 08/620,280, filed March 22, 1996, now
abandoned; which is a continuation-in-part of U.S. Application No. 08/532,136, filed
September 22, 1995, now abandoned; which is a continuation of U.S. Application
15 No. 08/523,435, filed September 1, 1995, now abandoned.

TECHNICAL FIELD

The present invention relates generally to the detection of
Mycobacterium tuberculosis infection. The invention is more particularly related to
20 polypeptides comprising a *Mycobacterium tuberculosis* antigen, or a portion or other
variant thereof, and the use of such polypeptides for the serodiagnosis of
Mycobacterium tuberculosis infection.

BACKGROUND OF THE INVENTION

25 Tuberculosis is a chronic, infectious disease, that is generally caused by
infection with *Mycobacterium tuberculosis*. It is a major disease in developing
countries, as well as an increasing problem in developed areas of the world, with about
8 million new cases and 3 million deaths each year. Although the infection may be
asymptomatic for a considerable period of time, the disease is most commonly

manifested as an acute inflammation of the lungs, resulting in fever and a nonproductive cough. If left untreated, serious complications and death typically result.

Although tuberculosis can generally be controlled using extended antibiotic therapy, such treatment is not sufficient to prevent the spread of the disease.

5 Infected individuals may be asymptomatic, but contagious, for some time. In addition, although compliance with the treatment regimen is critical, patient behavior is difficult to monitor. Some patients do not complete the course of treatment, which can lead to ineffective treatment and the development of drug resistance.

Inhibiting the spread of tuberculosis will require effective vaccination

10 and accurate, early diagnosis of the disease. Currently, vaccination with live bacteria is the most efficient method for inducing protective immunity. The most common *Mycobacterium* for this purpose is *Bacillus Calmette-Guerin* (BCG), an avirulent strain of *Mycobacterium bovis*. However, the safety and efficacy of BCG is a source of controversy and some countries, such as the United States, do not vaccinate the general

15 public. Diagnosis is commonly achieved using a skin test, which involves intradermal exposure to tuberculin PPD (protein-purified derivative). Antigen-specific T cell responses result in measurable incubation at the injection site by 48-72 hours after injection, which indicates exposure to *Mycobacterial* antigens. Sensitivity and specificity have, however, been a problem with this test, and individuals vaccinated

20 with BCG cannot be distinguished from infected individuals.

While macrophages have been shown to act as the principal effectors of *M. tuberculosis* immunity, T cells are the predominant inducers of such immunity. The essential role of T cells in protection against *M. tuberculosis* infection is illustrated by the frequent occurrence of *M. tuberculosis* in AIDS patients, due to the depletion of

25 CD4 T cells associated with human immunodeficiency virus (HIV) infection. *Mycobacterium*-reactive CD4 T cells have been shown to be potent producers of gamma-interferon (IFN- γ), which, in turn, has been shown to trigger the anti-mycobacterial effects of macrophages in mice. While the role of IFN- γ in humans is less clear, studies have shown that 1,25-dihydroxy-vitamin D₃, either alone or in

30 combination with IFN- γ or tumor necrosis factor-alpha, activates human macrophages

to inhibit *M. tuberculosis* infection. Furthermore, it is known that IFN- γ stimulates human macrophages to make 1,25-dihydroxy-vitamin D3. Similarly, IL-12 has been shown to play a role in stimulating resistance to *M. tuberculosis* infection. For a review of the immunology of *M. tuberculosis* infection see Chan and Kaufmann, in
5 *Tuberculosis: Pathogenesis, Protection and Control*, Bloom (ed.), ASM Press, Washington, DC, 1994.

Accordingly, there is a need in the art for improved diagnostic methods for detecting tuberculosis. The present invention fulfills this need and further provides other related advantages.

10

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for diagnosing tuberculosis. In one aspect, polypeptides are provided comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of such an antigen
15 that differs only in conservative substitutions and/or modifications. In one embodiment of this aspect, the soluble antigen has one of the following N-terminal sequences:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 115);
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 116);
20
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 117);
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 118);
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val (SEQ ID NO: 119);
25
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 120);
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser (SEQ ID NO: 121);
30

- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 122);
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn (SEQ ID NO: 123);
- (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID NO: 129)
- (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID NO: 130) or
- (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID NO: 131)

wherein Xaa may be any amino acid.

In a related aspect, polypeptides are provided comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications, the antigen having one of the following N-terminal sequences:

- (m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132) or
- (n) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID NO: 124)

wherein Xaa may be any amino acid.

In another embodiment, the soluble *M. tuberculosis* antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96 or a complement thereof under moderately stringent conditions.

In a related aspect, the polypeptides comprise an antigenic portion of a *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative

substitutions and/or modifications, wherein the antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 184-188, 194-196, 198, 210-220, 232, 234, 235, 237-242, 248-251, 256-271, 287, 288, 290-293 and 298-337, ,
5 the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 184-188, 194-196, 198, 210-220, 232, 234, 235, 237-242, 248-251, 256-271, 287, 288, 290-293 and 298-337, or a complement thereof under moderately stringent conditions.

In related aspects, DNA sequences encoding the above polypeptides.
10 recombinant expression vectors comprising these DNA sequences and host cells transformed or transfected with such expression vectors are also provided.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known *M. tuberculosis* antigen.

15 In further aspects of the subject invention, methods and diagnostic kits are provided for detecting tuberculosis in a patient. The methods comprise: (a) contacting a biological sample with at least one of the above polypeptides; and (b) detecting in the sample the presence of antibodies that bind to the polypeptide or polypeptides. thereby detecting *M. tuberculosis* infection in the biological sample.
20 Suitable biological samples include whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine. The diagnostic kits comprise one or more of the above polypeptides in combination with a detection reagent.

The present invention also provides methods for detecting *M. tuberculosis* infection comprising: (a) obtaining a biological sample from a patient;
25 (b) contacting the sample with at least one oligonucleotide primer in a polymerase chain reaction, the oligonucleotide primer being specific for a DNA sequence encoding the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In one embodiment, the oligonucleotide primer comprises at least about 10 contiguous nucleotides of such a
30 DNA sequence.

In a further aspect, the present invention provides a method for detecting *M. tuberculosis* infection in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA sequence encoding the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. In one embodiment, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of such a DNA sequence.

In yet another aspect, the present invention provides antibodies, both polyclonal and monoclonal, that bind to the polypeptides described above, as well as methods for their use in the detection of *M. tuberculosis* infection.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

15

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1A and B illustrate the stimulation of proliferation and interferon- γ production in T cells derived from a first and a second *M. tuberculosis*-immune donor, respectively, by the 14 Kd, 20 Kd and 26 Kd antigens described in Example 1.

Figures 2A-D illustrate the reactivity of antisera raised against secretory *M. tuberculosis* proteins, the known *M. tuberculosis* antigen 85b and the inventive antigens Tb38-1 and TbH-9, respectively, with *M. tuberculosis* lysate (lane 2), *M. tuberculosis* secretory proteins (lane 3), recombinant Tb38-1 (lane 4), recombinant TbH-9 (lane 5) and recombinant 85b (lane 5).

Figure 3A illustrates the stimulation of proliferation in a TbH-9-specific T cell clone by secretory *M. tuberculosis* proteins, recombinant TbH-9 and a control antigen, TbRa11.

Figure 3B illustrates the stimulation of interferon- γ production in a TbH-9-specific T cell clone by secretory *M. tuberculosis* proteins, PPD and recombinant TbH-9.

Figure 4 illustrates the reactivity of two representative polypeptides with sera from *M. tuberculosis*-infected and uninfected individuals, as compared to the reactivity of bacterial lysate.

Figure 5 shows the reactivity of four representative polypeptides with
5 sera from *M. tuberculosis*-infected and uninfected individuals, as compared to the reactivity of the 38 kD antigen.

Figure 6 shows the reactivity of recombinant 38 kD and TbRa11 antigens with sera from *M. tuberculosis* patients, PPD positive donors and normal donors.

10 Figure 7 shows the reactivity of the antigen TbRa2A with 38 kD negative sera.

Figure 8 shows the reactivity of the antigen of SEQ ID NO: 60 with sera from *M. tuberculosis* patients and normal donors.

Figure 9 illustrates the reactivity of the recombinant antigen TbH-29
15 (SEQ ID NO: 137) with sera from *M. tuberculosis* patients, PPD positive donors and normal donors as determined by indirect ELISA.

Figure 10 illustrates the reactivity of the recombinant antigen TbH-33 (SEQ ID NO: 140) with sera from *M. tuberculosis* patients and from normal donors, and with a pool of sera from *M. tuberculosis* patients, as determined both by direct and
20 indirect ELISA

Figure 11 illustrates the reactivity of increasing concentrations of the recombinant antigen TbH-33 (SEQ ID NO: 140) with sera from *M. tuberculosis* patients and from normal donors as determined by ELISA.

Figures 12A-E illustrate the reactivity of the recombinant antigens MO-
25 1, MO-2, MO-4, MO-28 and MO-29, respectively, with sera from *M. tuberculosis* patients and from normal donors as determined by ELISA.

SEQ. ID NO. 1 is the DNA sequence of TbRa1.

SEQ. ID NO. 2 is the DNA sequence of TbRa10.

30 SEQ. ID NO. 3 is the DNA sequence of TbRa11.

SEQ. ID NO. 4 is the DNA sequence of TbRa12.
SEQ. ID NO. 5 is the DNA sequence of TbRa13.
SEQ. ID NO. 6 is the DNA sequence of TbRa16.
SEQ. ID NO. 7 is the DNA sequence of TbRa17.
5 SEQ. ID NO. 8 is the DNA sequence of TbRa18.
SEQ. ID NO. 9 is the DNA sequence of TbRa19.
SEQ. ID NO. 10 is the DNA sequence of TbRa24.
SEQ. ID NO. 11 is the DNA sequence of TbRa26.
SEQ. ID NO. 12 is the DNA sequence of TbRa28.
10 SEQ. ID NO. 13 is the DNA sequence of TbRa29.
SEQ. ID NO. 14 is the DNA sequence of TbRa2A.
SEQ. ID NO. 15 is the DNA sequence of TbRa3.
SEQ. ID NO. 16 is the DNA sequence of TbRa32.
SEQ. ID NO. 17 is the DNA sequence of TbRa35.
15 SEQ. ID NO. 18 is the DNA sequence of TbRa36.
SEQ. ID NO. 19 is the DNA sequence of TbRa4.
SEQ. ID NO. 20 is the DNA sequence of TbRa9.
SEQ. ID NO. 21 is the DNA sequence of TbRaB.
SEQ. ID NO. 22 is the DNA sequence of TbRaC.
20 SEQ. ID NO. 23 is the DNA sequence of TbRaD.
SEQ. ID NO. 24 is the DNA sequence of YYWCPG.
SEQ. ID NO. 25 is the DNA sequence of AAMK.
SEQ. ID NO. 26 is the DNA sequence of TbL-23.
SEQ. ID NO. 27 is the DNA sequence of TbL-24.
25 SEQ. ID NO. 28 is the DNA sequence of TbL-25.
SEQ. ID NO. 29 is the DNA sequence of TbL-28.
SEQ. ID NO. 30 is the DNA sequence of TbL-29.
SEQ. ID NO. 31 is the DNA sequence of TbH-5.
SEQ. ID NO. 32 is the DNA sequence of TbH-8.
30 SEQ. ID NO. 33 is the DNA sequence of TbH-9.

- SEQ. ID NO. 34 is the DNA sequence of TbM-1.
SEQ. ID NO. 35 is the DNA sequence of TbM-3.
SEQ. ID NO. 36 is the DNA sequence of TbM-6.
SEQ. ID NO. 37 is the DNA sequence of TbM-7.
5 SEQ. ID NO. 38 is the DNA sequence of TbM-9.
SEQ. ID NO. 39 is the DNA sequence of TbM-12.
SEQ. ID NO. 40 is the DNA sequence of TbM-13.
SEQ. ID NO. 41 is the DNA sequence of TbM-14.
SEQ. ID NO. 42 is the DNA sequence of TbM-15.
10 SEQ. ID NO. 43 is the DNA sequence of TbH-4.
SEQ. ID NO. 44 is the DNA sequence of TbH-4-FWD.
SEQ. ID NO. 45 is the DNA sequence of TbH-12.
SEQ. ID NO. 46 is the DNA sequence of Tb38-1.
SEQ. ID NO. 47 is the DNA sequence of Tb38-4.
15 SEQ. ID NO. 48 is the DNA sequence of TbL-17.
SEQ. ID NO. 49 is the DNA sequence of TbL-20.
SEQ. ID NO. 50 is the DNA sequence of TbL-21.
SEQ. ID NO. 51 is the DNA sequence of TbH-16.
SEQ. ID NO. 52 is the DNA sequence of DPEP.
20 SEQ. ID NO. 53 is the deduced amino acid sequence of DPEP.
SEQ. ID NO. 54 is the protein sequence of DPV N-terminal Antigen.
SEQ. ID NO. 55 is the protein sequence of AVGS N-terminal Antigen.
SEQ. ID NO. 56 is the protein sequence of AAMK N-terminal Antigen.
SEQ. ID NO. 57 is the protein sequence of YYWC N-terminal Antigen.
25 SEQ. ID NO. 58 is the protein sequence of DIGS N-terminal Antigen.
SEQ. ID NO. 59 is the protein sequence of AEES N-terminal Antigen.
SEQ. ID NO. 60 is the protein sequence of DPEP N-terminal Antigen.
SEQ. ID NO. 61 is the protein sequence of APKT N-terminal Antigen.
SEQ. ID NO. 62 is the protein sequence of DPAS N-terminal Antigen.
30 SEQ. ID NO. 63 is the deduced amino acid sequence of TbM-1 Peptide.

SEQ. ID NO. 64 is the deduced amino acid sequence of TbRa1.
SEQ. ID NO. 65 is the deduced amino acid sequence of TbRa10.
SEQ. ID NO. 66 is the deduced amino acid sequence of TbRa11.
SEQ. ID NO. 67 is the deduced amino acid sequence of TbRa12.
5 SEQ. ID NO. 68 is the deduced amino acid sequence of TbRa13.
SEQ. ID NO. 69 is the deduced amino acid sequence of TbRa16.
SEQ. ID NO. 70 is the deduced amino acid sequence of TbRa17.
SEQ. ID NO. 71 is the deduced amino acid sequence of TbRa18.
SEQ. ID NO. 72 is the deduced amino acid sequence of TbRa19.
10 SEQ. ID NO. 73 is the deduced amino acid sequence of TbRa24.
SEQ. ID NO. 74 is the deduced amino acid sequence of TbRa26.
SEQ. ID NO. 75 is the deduced amino acid sequence of TbRa28.
SEQ. ID NO. 76 is the deduced amino acid sequence of TbRa29.
SEQ. ID NO. 77 is the deduced amino acid sequence of TbRa2A.
15 SEQ. ID NO. 78 is the deduced amino acid sequence of TbRa3.
SEQ. ID NO. 79 is the deduced amino acid sequence of TbRa32.
SEQ. ID NO. 80 is the deduced amino acid sequence of TbRa35.
SEQ. ID NO. 81 is the deduced amino acid sequence of TbRa36.
SEQ. ID NO. 82 is the deduced amino acid sequence of TbRa4.
20 SEQ. ID NO. 83 is the deduced amino acid sequence of TbRa9.
SEQ. ID NO. 84 is the deduced amino acid sequence of TbRaB.
SEQ. ID NO. 85 is the deduced amino acid sequence of TbRaC.
SEQ. ID NO. 86 is the deduced amino acid sequence of TbRaD.
SEQ. ID NO. 87 is the deduced amino acid sequence of YYWCPG.
25 SEQ. ID NO. 88 is the deduced amino acid sequence of TbAAMK.
SEQ. ID NO. 89 is the deduced amino acid sequence of Tb38-1.
SEQ. ID NO. 90 is the deduced amino acid sequence of TbH-4.
SEQ. ID NO. 91 is the deduced amino acid sequence of TbH-8.
SEQ. ID NO. 92 is the deduced amino acid sequence of TbH-9.
30 SEQ. ID NO. 93 is the deduced amino acid sequence of TbH-12.

- SEQ. ID NO. 94 is the DNA sequence of DPAS.
- SEQ. ID NO. 95 is the deduced amino acid sequence of DPAS.
- SEQ. ID NO. 96 is the DNA sequence of DPV.
- SEQ. ID NO. 97 is the deduced amino acid sequence of DPV.
- 5 SEQ. ID NO. 98 is the DNA sequence of ESAT-6.
- SEQ. ID NO. 99 is the deduced amino acid sequence of ESAT-6.
- SEQ. ID NO. 100 is the DNA sequence of TbH-8-2.
- SEQ. ID NO. 101 is the DNA sequence of TbH-9FL.
- SEQ. ID NO. 102 is the deduced amino acid sequence of TbH-9FL.
- 10 SEQ. ID NO. 103 is the DNA sequence of TbH-9-1.
- SEQ. ID NO. 104 is the deduced amino acid sequence of TbH-9-1.
- SEQ. ID NO. 105 is the DNA sequence of TbH-9-4.
- SEQ. ID NO. 106 is the deduced amino acid sequence of TbH-9-4.
- SEQ. ID NO. 107 is the DNA sequence of Tb38-1F2 IN.
- 15 SEQ. ID NO. 108 is the DNA sequence of Tb38-1F2 RP.
- SEQ. ID NO. 109 is the deduced amino acid sequence of Tb37-FL.
- SEQ. ID NO. 110 is the deduced amino acid sequence of Tb38-IN.
- SEQ. ID NO. 111 is the DNA sequence of Tb38-1F3.
- SEQ. ID NO. 112 is the deduced amino acid sequence of Tb38-1F3.
- 20 SEQ. ID NO. 113 is the DNA sequence of Tb38-1F5.
- SEQ. ID NO. 114 is the DNA sequence of Tb38-1F6.
- SEQ. ID NO. 115 is the deduced N-terminal amino acid sequence of DPV.
- SEQ. ID NO. 116 is the deduced N-terminal amino acid sequence of AVGS.
- SEQ. ID NO. 117 is the deduced N-terminal amino acid sequence of AAMK.
- 25 SEQ. ID NO. 118 is the deduced N-terminal amino acid sequence of YYWC.
- SEQ. ID NO. 119 is the deduced N-terminal amino acid sequence of DIGS.
- SEQ. ID NO. 120 is the deduced N-terminal amino acid sequence of AAES.
- SEQ. ID NO. 121 is the deduced N-terminal amino acid sequence of DPEP.
- SEQ. ID NO. 122 is the deduced N-terminal amino acid sequence of APKT.
- 30 SEQ. ID NO. 123 is the deduced N-terminal amino acid sequence of DPAS.

SEQ. ID NO. 124 is the protein sequence of DPPD N-terminal Antigen.

SEQ ID NO. 125-128 are the protein sequences of four DPPD cyanogen bromide fragments.

SEQ ID NO. 129 is the N-terminal protein sequence of XDS antigen.

5 SEQ ID NO. 130 is the N-terminal protein sequence of AGD antigen.

SEQ ID NO. 131 is the N-terminal protein sequence of APE antigen.

SEQ ID NO. 132 is the N-terminal protein sequence of XYI antigen.

SEQ ID NO. 133 is the DNA sequence of TbH-29.

SEQ ID NO. 134 is the DNA sequence of TbH-30.

10 SEQ ID NO. 135 is the DNA sequence of TbH-32.

SEQ ID NO. 136 is the DNA sequence of TbH-33.

SEQ ID NO. 137 is the predicted amino acid sequence of TbH-29.

SEQ ID NO. 138 is the predicted amino acid sequence of TbH-30.

SEQ ID NO. 139 is the predicted amino acid sequence of TbH-32.

15 SEQ ID NO. 140 is the predicted amino acid sequence of TbH-33.

SEQ ID NO: 141-146 are PCR primers used in the preparation of a fusion protein containing TbRa3, 38 kD and Tb38-1.

SEQ ID NO: 147 is the DNA sequence of the fusion protein containing TbRa3, 38 kD and Tb38-1.

20 SEQ ID NO: 148 is the amino acid sequence of the fusion protein containing TbRa3, 38 kD and Tb38-1.

SEQ ID NO: 149 is the DNA sequence of the M. tuberculosis antigen 38 kD.

SEQ ID NO: 150 is the amino acid sequence of the M. tuberculosis antigen 38 kD.

25 SEQ ID NO: 151 is the DNA sequence of XP14.

SEQ ID NO: 152 is the DNA sequence of XP24.

SEQ ID NO: 153 is the DNA sequence of XP31.

SEQ ID NO: 154 is the 5' DNA sequence of XP32.

SEQ ID NO: 155 is the 3' DNA sequence of XP32.

30 SEQ ID NO: 156 is the predicted amino acid sequence of XP14.

SEQ ID NO: 157 is the predicted amino acid sequence encoded by the reverse complement of XP14.

SEQ ID NO: 158 is the DNA sequence of XP27.

SEQ ID NO: 159 is the DNA sequence of XP36.

5 SEQ ID NO: 160 is the 5' DNA sequence of XP4.

SEQ ID NO: 161 is the 5' DNA sequence of XP5.

SEQ ID NO: 162 is the 5' DNA sequence of XP17.

SEQ ID NO: 163 is the 5' DNA sequence of XP30.

SEQ ID NO: 164 is the 5' DNA sequence of XP2.

10 SEQ ID NO: 165 is the 3' DNA sequence of XP2.

SEQ ID NO: 166 is the 5' DNA sequence of XP3.

SEQ ID NO: 167 is the 3' DNA sequence of XP3.

SEQ ID NO: 168 is the 5' DNA sequence of XP6.

SEQ ID NO: 169 is the 3' DNA sequence of XP6.

15 SEQ ID NO: 170 is the 5' DNA sequence of XP18.

SEQ ID NO: 171 is the 3' DNA sequence of XP18.

SEQ ID NO: 172 is the 5' DNA sequence of XP19.

SEQ ID NO: 173 is the 3' DNA sequence of XP19.

SEQ ID NO: 174 is the 5' DNA sequence of XP22.

20 SEQ ID NO: 175 is the 3' DNA sequence of XP22.

SEQ ID NO: 176 is the 5' DNA sequence of XP25.

SEQ ID NO: 177 is the 3' DNA sequence of XP25.

SEQ ID NO: 178 is the full-length DNA sequence of TbH4-XP1.

SEQ ID NO: 179 is the predicted amino acid sequence of TbH4-XP1.

25 SEQ ID NO: 180 is the predicted amino acid sequence encoded by the reverse complement of TbH4-XP1.

SEQ ID NO: 181 is a first predicted amino acid sequence encoded by XP36.

SEQ ID NO: 182 is a second predicted amino acid sequence encoded by XP36.

30 SEQ ID NO: 183 is the predicted amino acid sequence encoded by the reverse complement of XP36.

- SEQ ID NO: 184 is the DNA sequence of RDIF2.
- SEQ ID NO: 185 is the DNA sequence of RDIF5.
- SEQ ID NO: 186 is the DNA sequence of RDIF8.
- SEQ ID NO: 187 is the DNA sequence of RDIF10.
- 5 SEQ ID NO: 188 is the DNA sequence of RDIF11.
- SEQ ID NO: 189 is the predicted amino acid sequence of RDIF2.
- SEQ ID NO: 190 is the predicted amino acid sequence of RDIF5.
- SEQ ID NO: 191 is the predicted amino acid sequence of RDIF8.
- SEQ ID NO: 192 is the predicted amino acid sequence of RDIF10.
- 10 SEQ ID NO: 193 is the predicted amino acid sequence of RDIF11.
- SEQ ID NO: 194 is the 5' DNA sequence of RDIF12.
- SEQ ID NO: 195 is the 3' DNA sequence of RDIF12.
- SEQ ID NO: 196 is the DNA sequence of RDIF7.
- SEQ ID NO: 197 is the predicted amino acid sequence of RDIF7.
- 15 SEQ ID NO: 198 is the DNA sequence of DIF2-1.
- SEQ ID NO: 199 is the predicted amino acid sequence of DIF2-1.
- SEQ ID NO: 200-207 are PCR primers used in the preparation of a fusion protein containing TbRa5, 38 kD, Tb38-1 and DPEP (hereinafter referred to as TbF-2).
- 20 SEQ ID NO: 208 is the DNA sequence of the fusion protein TbF-2.
- SEQ ID NO: 209 is the amino acid sequence of the fusion protein TbF-2.
- SEQ ID NO: 210 is the 5' DNA sequence of MO-1.
- SEQ ID NO: 211 is the 5' DNA sequence for MO-2.
- SEQ ID NO: 212 is the 5' DNA sequence for MO-4.
- 25 SEQ ID NO: 213 is the 5' DNA sequence for MO-8.
- SEQ ID NO: 214 is the 5' DNA sequence for MO-9.
- SEQ ID NO: 215 is the 5' DNA sequence for MO-26.
- SEQ ID NO: 216 is the 5' DNA sequence for MO-28.
- SEQ ID NO: 217 is the 5' DNA sequence for MO-29.
- 30 SEQ ID NO: 218 is the 5' DNA sequence for MO-30.

SEQ ID NO: 219 is the 5' DNA sequence for MO-34.
SEQ ID NO: 220 is the 5' DNA sequence for MO-35.
SEQ ID NO: 221 is the predicted amino acid sequence for MO-1.
SEQ ID NO: 222 is the predicted amino acid sequence for MO-2.
5 SEQ ID NO: 223 is the predicted amino acid sequence for MO-4.
SEQ ID NO: 224 is the predicted amino acid sequence for MO-8.
SEQ ID NO: 225 is the predicted amino acid sequence for MO-9.
SEQ ID NO: 226 is the predicted amino acid sequence for MO-26.
SEQ ID NO: 227 is the predicted amino acid sequence for MO-28.
10 SEQ ID NO: 228 is the predicted amino acid sequence for MO-29.
SEQ ID NO: 229 is the predicted amino acid sequence for MO-30.
SEQ ID NO: 230 is the predicted amino acid sequence for MO-34.
SEQ ID NO: 231 is the predicted amino acid sequence for MO-35.
SEQ ID NO: 232 is the determined DNA sequence for MO-10.
15 SEQ ID NO: 233 is the predicted amino acid sequence for MO-10.
SEQ ID NO: 234 is the 3' DNA sequence for MO-27.
SEQ ID NO: 235 is the full-length DNA sequence for DPPD.
SEQ ID NO: 236 is the predicted full-length amino acid sequence for DPPD
SEQ ID NO: 237 is the determined 5' cDNA sequence for LSER-10
20 SEQ ID NO: 238 is the determined 5' cDNA sequence for LSER-11
SEQ ID NO: 239 is the determined 5' cDNA sequence for LSER-12
SEQ ID NO: 240 is the determined 5' cDNA sequence for LSER-13
SEQ ID NO: 241 is the determined 5' cDNA sequence for LSER-16
SEQ ID NO: 242 is the determined 5' cDNA sequence for LSER-25
25 SEQ ID NO: 243 is the predicted amino acid sequence for LSER-10
SEQ ID NO: 244 is the predicted amino acid sequence for LSER-12
SEQ ID NO: 245 is the predicted amino acid sequence for LSER-13
SEQ ID NO: 246 is the predicted amino acid sequence for LSER-16
SEQ ID NO: 247 is the predicted amino acid sequence for LSER-25
30 SEQ ID NO: 248 is the determined cDNA sequence for LSER-18

SEQ ID NO: 249 is the determined cDNA sequence for LSER-23
SEQ ID NO: 250 is the determined cDNA sequence for LSER-24
SEQ ID NO: 251 is the determined cDNA sequence for LSER-27
SEQ ID NO: 252 is the predicted amino acid sequence for LSER-18
5 SEQ ID NO: 253 is the predicted amino acid sequence for LSER-23
SEQ ID NO: 254 is the predicted amino acid sequence for LSER-24
SEQ ID NO: 255 is the predicted amino acid sequence for LSER-27
SEQ ID NO: 256 is the determined 5' cDNA sequence for LSER-1
SEQ ID NO: 257 is the determined 5' cDNA sequence for LSER-3
10 SEQ ID NO: 258 is the determined 5' cDNA sequence for LSER-4
SEQ ID NO: 259 is the determined 5' cDNA sequence for LSER-5
SEQ ID NO: 260 is the determined 5' cDNA sequence for LSER-6
SEQ ID NO: 261 is the determined 5' cDNA sequence for LSER-8
SEQ ID NO: 262 is the determined 5' cDNA sequence for LSER-14
15 SEQ ID NO: 263 is the determined 5' cDNA sequence for LSER-15
SEQ ID NO: 264 is the determined 5' cDNA sequence for LSER-17
SEQ ID NO: 265 is the determined 5' cDNA sequence for LSER-19
SEQ ID NO: 266 is the determined 5' cDNA sequence for LSER-20
SEQ ID NO: 267 is the determined 5' cDNA sequence for LSER-22
20 SEQ ID NO: 268 is the determined 5' cDNA sequence for LSER-26
SEQ ID NO: 269 is the determined 5' cDNA sequence for LSER-28
SEQ ID NO: 270 is the determined 5' cDNA sequence for LSER-29
SEQ ID NO: 271 is the determined 5' cDNA sequence for LSER-30
SEQ ID NO: 272 is the predicted amino acid sequence for LSER-1
25 SEQ ID NO: 273 is the predicted amino acid sequence for LSER-3
SEQ ID NO: 274 is the predicted amino acid sequence for LSER-5
SEQ ID NO: 275 is the predicted amino acid sequence for LSER-6
SEQ ID NO: 276 is the predicted amino acid sequence for LSER-8
SEQ ID NO: 277 is the predicted amino acid sequence for LSER-14
30 SEQ ID NO: 278 is the predicted amino acid sequence for LSER-15

SEQ ID NO: 279 is the predicted amino acid sequence for LSER-17
SEQ ID NO: 280 is the predicted amino acid sequence for LSER-19
SEQ ID NO: 281 is the predicted amino acid sequence for LSER-20
SEQ ID NO: 282 is the predicted amino acid sequence for LSER-22
5 SEQ ID NO: 283 is the predicted amino acid sequence for LSER-26
SEQ ID NO: 284 is the predicted amino acid sequence for LSER-28
SEQ ID NO: 285 is the predicted amino acid sequence for LSER-29
SEQ ID NO: 286 is the predicted amino acid sequence for LSER-30
SEQ ID NO: 287 is the determined cDNA sequence for LSER-9
10 SEQ ID NO: 288 is the determined cDNA sequence for the reverse complement
of LSER-6
SEQ ID NO: 289 is the predicted amino acid sequence for the reverse
complement of LSER-6
SEQ ID NO: 290 is the determined 5' cDNA sequence for MO-12
15 SEQ ID NO: 291 is the determined 5' cDNA sequence for MO-13
SEQ ID NO: 292 is the determined 5' cDNA sequence for MO-19
SEQ ID NO: 293 is the determined 5' cDNA sequence for MO-39
SEQ ID NO: 294 is the predicted amino acid sequence for MO-12
SEQ ID NO: 295 is the predicted amino acid sequence for MO-13
20 SEQ ID NO: 296 is the predicted amino acid sequence for MO-19
SEQ ID NO: 297 is the predicted amino acid sequence for MO-39
SEQ ID NO: 298 is the determined 5' cDNA sequence for Erdsn-1
SEQ ID NO: 299 is the determined 5' cDNA sequence for Erdsn-2
SEQ ID NO: 300 is the determined 5' cDNA sequence for Erdsn-4
25 SEQ ID NO: 301 is the determined 5' cDNA sequence for Erdsn-5
SEQ ID NO: 302 is the determined 5' cDNA sequence for Erdsn-6
SEQ ID NO: 303 is the determined 5' cDNA sequence for Erdsn-7
SEQ ID NO: 304 is the determined 5' cDNA sequence for Erdsn-8
SEQ ID NO: 305 is the determined 5' cDNA sequence for Erdsn-9
30 SEQ ID NO: 306 is the determined 5' cDNA sequence for Erdsn-10

SEQ ID NO: 307 is the determined 5' cDNA sequence for Erdsn-12
SEQ ID NO: 308 is the determined 5' cDNA sequence for Erdsn-13
SEQ ID NO: 309 is the determined 5' cDNA sequence for Erdsn-14
SEQ ID NO: 310 is the determined 5' cDNA sequence for Erdsn-15
5 SEQ ID NO: 311 is the determined 5' cDNA sequence for Erdsn-16
SEQ ID NO: 312 is the determined 5' cDNA sequence for Erdsn-17
SEQ ID NO: 313 is the determined 5' cDNA sequence for Erdsn-18
SEQ ID NO: 314 is the determined 5' cDNA sequence for Erdsn-21
SEQ ID NO: 315 is the determined 5' cDNA sequence for Erdsn-22
10 SEQ ID NO: 316 is the determined 5' cDNA sequence for Erdsn-23
SEQ ID NO: 317 is the determined 5' cDNA sequence for Erdsn-25
SEQ ID NO: 318 is the determined 3' cDNA sequence for Erdsn-1
SEQ ID NO: 319 is the determined 3' cDNA sequence for Erdsn-2
SEQ ID NO: 320 is the determined 3' cDNA sequence for Erdsn-4
15 SEQ ID NO: 321 is the determined 3' cDNA sequence for Erdsn-5
SEQ ID NO: 322 is the determined 3' cDNA sequence for Erdsn-7
SEQ ID NO: 323 is the determined 3' cDNA sequence for Erdsn-8
SEQ ID NO: 324 is the determined 3' cDNA sequence for Erdsn-9
SEQ ID NO: 325 is the determined 3' cDNA sequence for Erdsn-10
20 SEQ ID NO: 326 is the determined 3' cDNA sequence for Erdsn-12
SEQ ID NO: 327 is the determined 3' cDNA sequence for Erdsn-13
SEQ ID NO: 328 is the determined 3' cDNA sequence for Erdsn-14
SEQ ID NO: 329 is the determined 3' cDNA sequence for Erdsn-15
SEQ ID NO: 330 is the determined 3' cDNA sequence for Erdsn-16
25 SEQ ID NO: 331 is the determined 3' cDNA sequence for Erdsn-17
SEQ ID NO: 332 is the determined 3' cDNA sequence for Erdsn-18
SEQ ID NO: 333 is the determined 3' cDNA sequence for Erdsn-21
SEQ ID NO: 334 is the determined 3' cDNA sequence for Erdsn-22
SEQ ID NO: 335 is the determined 3' cDNA sequence for Erdsn-23
30 SEQ ID NO: 336 is the determined 3' cDNA sequence for Erdsn-25

- SEQ ID NO: 337 is the determined cDNA sequence for Erdsn-24
- SEQ ID NO: 338 is the determined amino acid sequence for a *M. tuberculosis* 85b precursor homolog
- SEQ ID NO: 339 is the determined amino acid sequence for spot 1
- 5 SEQ ID NO: 340 is a determined amino acid sequence for spot 2
- SEQ ID NO: 341 is a determined amino acid sequence for spot 2
- SEQ ID NO: 342 is the determined amino acid seq for spot 4
- SEQ ID NO: 343 is the sequence of primer PDM-157
- SEQ ID NO: 344 is the sequence of primer PDM-160
- 10 SEQ ID NO: 345 is the DNA sequence of the fusion protein TbF-6
- SEQ ID NO: 346 is the amino acid sequence of fusion protein TbF-6
- SEQ ID NO: 347 is the sequence of primer PDM-176
- SEQ ID NO: 348 is the sequence of primer PDM-175
- SEQ ID NO: 349 is the DNA sequence of the fusion protein TbF-8
- 15 SEQ ID NO: 350 is the amino acid sequence of the fusion protein TbF-8

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to

20 compositions and methods for diagnosing tuberculosis. The compositions of the subject invention include polypeptides that comprise at least one antigenic portion of a *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications. Polypeptides within the scope of the present invention include, but are not limited to, soluble *M. tuberculosis* antigens. A "soluble

25 *M. tuberculosis* antigen" is a protein of *M. tuberculosis* origin that is present in *M. tuberculosis* culture filtrate. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an antigenic portion of one of the above antigens may consist entirely of the

30 antigenic portion, or may contain additional sequences. The additional sequences may

be derived from the native *M. tuberculosis* antigen or may be heterologous, and such sequences may (but need not) be antigenic.

An "antigenic portion" of an antigen (which may or may not be soluble) is a portion that is capable of reacting with sera obtained from an *M. tuberculosis*-infected individual (i.e., generates an absorbance reading with sera from infected individuals that is at least three standard deviations above the absorbance obtained with sera from uninfected individuals, in a representative ELISA assay described herein). An "*M. tuberculosis*-infected individual" is a human who has been infected with *M. tuberculosis* (e.g., has an intradermal skin test response to PPD that is at least 0.5 cm in diameter). Infected individuals may display symptoms of tuberculosis or may be free of disease symptoms. Polypeptides comprising at least an antigenic portion of one or more *M. tuberculosis* antigens as described herein may generally be used, alone or in combination, to detect tuberculosis in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of tuberculosis. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and

hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

5 Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs
10 transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited
15 nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide
20 sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recite nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight;
25 followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

In a related aspect, combination, or fusion, polypeptides are disclosed. A "fusion polypeptide" is a polypeptide comprising at least one of the above antigenic portions and one or more additional antigenic *M. tuberculosis* sequences, which are
30 joined via a peptide linkage into a single amino acid chain. The sequences may be

joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linker sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the antigenic properties of the component polypeptides.

In general, *M. tuberculosis* antigens, and DNA sequences encoding such
5 antigens, may be prepared using any of a variety of procedures. For example, soluble antigens may be isolated from *M. tuberculosis* culture filtrate by procedures known to those of ordinary skill in the art, including anion-exchange and reverse phase chromatography. Purified antigens may then be evaluated for a desired property, such as the ability to react with sera obtained from an *M. tuberculosis*-infected individual.
10 Such screens may be performed using the representative methods described herein. Antigens may then be partially sequenced using, for example, traditional Edman chemistry. See Edman and Berg, *Eur. J. Biochem.* 80:116-132, 1967.

Antigens may also be produced recombinantly using a DNA sequence that encodes the antigen, which has been inserted into an expression vector and
15 expressed in an appropriate host. DNA molecules encoding soluble antigens may be isolated by screening an appropriate *M. tuberculosis* expression library with anti-sera (*e.g.*, rabbit) raised specifically against soluble *M. tuberculosis* antigens. DNA sequences encoding antigens that may or may not be soluble may be identified by screening an appropriate *M. tuberculosis* genomic or cDNA expression library with sera
20 obtained from patients infected with *M. tuberculosis*. Such screens may generally be performed using techniques well known in the art, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989.

DNA sequences encoding soluble antigens may also be obtained by
25 screening an appropriate *M. tuberculosis* cDNA or genomic DNA library for DNA sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated soluble antigens. Degenerate oligonucleotide sequences for use in such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*,
30 Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (and references cited

therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a cDNA or genomic library. The library screen may then be performed using the isolated probe.

5 Regardless of the method of preparation, the antigens described herein are "antigenic." More specifically, the antigens have the ability to react with sera obtained from an *M. tuberculosis*-infected individual. Reactivity may be evaluated using, for example, the representative ELISA assays described herein, where an absorbance reading with sera from infected individuals that is at least three standard
10 deviations above the absorbance obtained with sera from uninfected individuals is considered positive.

 Antigenic portions of *M. tuberculosis* antigens may be prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited
15 therein. Such techniques include screening polypeptide portions of the native antigen for antigenic properties. The representative ELISAs described herein may generally be employed in these screens. An antigenic portion of a polypeptide is a portion that, within such representative assays, generates a signal in such assays that is substantially similar to that generated by the full length antigen. In other words, an antigenic portion
20 of a *M. tuberculosis* antigen generates at least about 20%, and preferably about 100%, of the signal induced by the full length antigen in a model ELISA as described herein.

 Portions and other variants of *M. tuberculosis* antigens may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated
25 using techniques well known in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from
30 suppliers such as Applied BioSystems, Inc., Foster City, CA, and may be operated

according to the manufacturer's instructions. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

5 Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a DNA sequence encoding the polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available
10 filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

 Any of a variety of expression vectors known to those of ordinary skill in
15 the art may be employed to express recombinant polypeptides as described herein. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian
20 cell line, such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

 In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form. Preferably, the polypeptides
25 are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure. For use in the methods described herein, however, such substantially pure polypeptides may be combined.

 In certain specific embodiments, the subject invention discloses polypeptides comprising at least an antigenic portion of a soluble *M. tuberculosis*

antigen (or a variant of such an antigen), where the antigen has one of the following N-terminal sequences:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 115);
- 5 (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 116);
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 117);
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 118);
- 10 (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val (SEQ ID NO: 119);
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 120);
- 15 (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser (SEQ ID NO: 121);
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 122);
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Gln-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn (SEQ ID NO: 123);
- 20 (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID NO: 129)
- (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID NO: 130) or
- 25 (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID NO: 131)

wherein Xaa may be any amino acid, preferably a cysteine residue. A DNA sequence encoding the antigen identified as (g) above is provided in SEQ ID NO: 52, the deduced amino acid sequence of which is provided in SEQ ID NO: 53. A DNA sequence

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encoding the antigen identified as (a) above is provided in SEQ ID NO: 96; its deduced amino acid sequence is provided in SEQ ID NO: 97. A DNA sequence corresponding to antigen (d) above is provided in SEQ ID NO: 24, a DNA sequence corresponding to antigen (c) is provided in SEQ ID NO: 25 and a DNA sequence corresponding to antigen (I) is disclosed in SEQ ID NO: 94 and its deduced amino acid sequence is provided in SEQ ID NO: 95.

In a further specific embodiment, the subject invention discloses polypeptides comprising at least an immunogenic portion of an *M. tuberculosis* antigen having one of the following N-terminal sequences, or a variant thereof that differs only in conservative substitutions and/or modifications:

(m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132) or

(n) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID NO: 124)

wherein Xaa may be any amino acid, preferably a cysteine residue. A DNA sequence encoding the antigen of (n) above is provided in SEQ ID NO: 235, with the corresponding predicted full-length amino acid sequence being provided in SEQ ID NO: 236.

In other specific embodiments, the subject invention discloses polypeptides comprising at least an antigenic portion of a soluble *M. tuberculosis* antigen (or a variant of such an antigen) that comprises one or more of the amino acid sequences encoded by (a) the DNA sequences of SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96. (b) the complements of such DNA sequences, or (c) DNA sequences substantially homologous to a sequence in (a) or (b).

In further specific embodiments, the subject invention discloses polypeptides comprising at least an antigenic portion of a *M. tuberculosis* antigen (or a variant of such an antigen), which may or may not be soluble, that comprises one or more of the amino acid sequences encoded by (a) the DNA sequences of SEQ ID NOS: 26-51, 133, 134, 158-178, 184-188, 194-196, 198, 210-220, 232, 234, 235, 237-

242, 248-251, 256-271, 287, 288, 290-293 and 298-337, (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b).

In a related aspect, the present invention provides fusion proteins
5 comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known *M. tuberculosis* antigen, such as the 38 kD antigen described in Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989, (Genbank Accession No. M30046) or ESAT-6 (SEQ ID NOS: 98 and 99), together with variants of such fusion proteins. The fusion proteins of the present invention may also include a
10 linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or
15 without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the
20 second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure
25 that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers
30 include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc.*

Natl. Acad. Sci. USA 83:8258-8562, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric hindrance.

In another aspect, the present invention provides methods for using the polypeptides described above to diagnose tuberculosis. In this aspect, methods are provided for detecting *M. tuberculosis* infection in a biological sample, using one or more of the above polypeptides, alone or in combination. In embodiments in which multiple polypeptides are employed, polypeptides other than those specifically described herein, such as the 38 kD antigen described in Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989, may be included. As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient or a blood supply. The polypeptide(s) are used in an assay, as described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample, relative to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to mycobacterial antigens which may be indicative of tuberculosis.

In embodiments in which more than one polypeptide is employed, the polypeptides used are preferably complementary (*i.e.*, one component polypeptide will tend to detect infection in samples where the infection would not be detected by another component polypeptide). Complementary polypeptides may generally be identified by using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *M. tuberculosis*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested. Such polypeptides are complementary. For example, approximately 25-30% of sera from tuberculosis-infected individuals are negative for antibodies to any single protein, such as the 38 kD antigen mentioned above. Complementary

polypeptides may, therefore, be used in combination with the 38 kD antigen to improve sensitivity of a diagnostic test.

There are a variety of assay formats known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. *See, e.g.,* 5 Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include 10 antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (*e.g.*, in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the 15 binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. 20 Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of 25 techniques known to those of ordinary skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to 30 a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may

be achieved by contacting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging
5 from about 10 ng to about 1 μ g, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the
10 polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent
15 assay (ELISA). This assay may be performed by first contacting a polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized
20 antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection reagent.

More specifically, once the polypeptide is immobilized on the support as described above, the remaining protein binding sites on the support are typically
25 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO) may be employed. The immobilized polypeptide is then incubated with the sample, and antibody is allowed to bind to the antigen. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an
30 appropriate contact time (*i.e.,* incubation time) is that period of time that is sufficient to

detect the presence of antibody within a *M. tuberculosis*-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily
5 determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. Detection reagent may then be added to the solid support. An appropriate detection reagent is any
10 compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the detection reagent contains a binding agent (such as, for example, Protein A, Protein G, immunoglobulin, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors,
15 inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups, biotin and colloidal particles, such as colloidal gold and selenium. The conjugation of binding agent to reporter group may be achieved using standard methods known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (e.g., Zymed Laboratories,
20 San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An appropriate amount of time may generally be determined from the manufacturer's instructions or by assaying the level of binding that occurs over a period of time.
25 Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin
30 may be detected using avidin, coupled to a different reporter group (commonly a

radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*M. tuberculosis* antibodies
5 in the sample, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above
10 the predetermined cut-off value is considered positive for tuberculosis. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive
15 rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the
20 cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for tuberculosis.

In a related embodiment, the assay is performed in a rapid flow-through
25 or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (*e.g.*, protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The
30 detection of bound detection reagent may then be performed as described above. In the

strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-
5 *M. tuberculosis* antibodies in the sample. Typically, the concentration of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be
10 sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (*e.g.*, one drop) of patient serum or blood.

Of course, numerous other assay protocols exist that are suitable for use
15 with the polypeptides of the present invention. The above descriptions are intended to be exemplary only.

In yet another aspect, the present invention provides antibodies to the inventive polypeptides. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A*
20 *Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response
25 may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example,
30 affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the
5 desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells
10 and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding
15 activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable
20 vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

25 Antibodies may be used in diagnostic tests to detect the presence of *M. tuberculosis* antigens using assays similar to those detailed above and other techniques well known to those of skill in the art, thereby providing a method for detecting *M. tuberculosis* infection in a patient.

Diagnostic reagents of the present invention may also comprise DNA
30 sequences encoding one or more of the above polypeptides, or one or more portions

thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify *M. tuberculosis*-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a polypeptide of the present invention.

- 5 The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a polypeptide of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

- 10 As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about
15 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Techniques for
20 both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect *M. tuberculosis*-specific sequences in biological samples. DNA probes or primers comprising oligonucleotide sequences described above may be used alone, in combination with each other, or with previously identified sequences, such as the 38 kD
25 antigen discussed above.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

PURIFICATION AND CHARACTERIZATION OF POLYPEPTIDES

5

FROM *M. TUBERCULOSIS* CULTURE FILTRATE

This example illustrates the preparation of *M. tuberculosis* soluble polypeptides from culture filtrate. Unless otherwise noted, all percentages in the following example are weight per volume.

10

M. tuberculosis (either H37Ra, ATCC No. 25177, or H37Rv, ATCC No. 25618) was cultured in sterile GAS media at 37°C for fourteen days. The media was then vacuum filtered (leaving the bulk of the cells) through a 0.45 μ filter into a sterile 2.5 L bottle. The media was then filtered through a 0.2 μ filter into a sterile 4 L bottle. NaN₃ was then added to the culture filtrate to a concentration of 0.04%. The bottles were then placed in a 4°C cold room.

15

The culture filtrate was concentrated by placing the filtrate in a 12 L reservoir that had been autoclaved and feeding the filtrate into a 400 ml Amicon stir cell which had been rinsed with ethanol and contained a 10,000 kDa MWCO membrane. The pressure was maintained at 60 psi using nitrogen gas. This procedure reduced the 12 L volume to approximately 50 ml.

20

The culture filtrate was then dialyzed into 0.1% ammonium bicarbonate using a 8,000 kDa MWCO cellulose ester membrane, with two changes of ammonium bicarbonate solution. Protein concentration was then determined by a commercially available BCA assay (Pierce, Rockford, IL).

25

The dialyzed culture filtrate was then lyophilized, and the polypeptides resuspended in distilled water. The polypeptides were then dialyzed against 0.01 mM 1.3 bis[tris(hydroxymethyl)-methylamino]propane, pH 7.5 (Bis-Tris propane buffer), the initial conditions for anion exchange chromatography. Fractionation was performed using gel perfusion chromatography on a POROS 146 II Q/M anion exchange column 4.6 mm x 100 mm (Perseptive BioSystems, Framingham, MA) equilibrated in 0.01 mM

30

Bis-Tris propane buffer pH 7.5. Polypeptides were eluted with a linear 0-0.5 M NaCl gradient in the above buffer system. The column eluent was monitored at a wavelength of 220 nm.

The pools of polypeptides eluting from the ion exchange column were
5 dialyzed against distilled water and lyophilized. The resulting material was dissolved in 0.1% trifluoroacetic acid (TFA) pH 1.9 in water, and the polypeptides were purified on a Delta-Pak C18 column (Waters, Milford, MA) 300 Angstrom pore size, 5 micron particle size (3.9 x 150 mm). The polypeptides were eluted from the column with a linear gradient from 0-60% dilution buffer (0.1% TFA in acetonitrile). The flow rate
10 was 0.75 ml/minute and the HPLC eluent was monitored at 214 nm. Fractions containing the eluted polypeptides were collected to maximize the purity of the individual samples. Approximately 200 purified polypeptides were obtained.

The purified polypeptides were then screened for the ability to induce T-cell proliferation in PBMC preparations. The PBMCs from donors known to be PPD
15 skin test positive and whose T cells were shown to proliferate in response to PPD and crude soluble proteins from MTB were cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 µg/ml gentamicin. Purified polypeptides were added in duplicate at concentrations of 0.5 to 10 µg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 µl, 50 µl of medium
20 was removed from each well for determination of IFN-γ levels, as described below. The plates were then pulsed with 1 µCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that resulted in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone were considered positive.

25 IFN-γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates were coated with a mouse monoclonal antibody directed to human IFN-γ (Chemicon) in PBS for four hours at room temperature. Wells were then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates were then washed six times in PBS/0.2% TWEEN-20 and
30 samples diluted 1:2 in culture medium in the ELISA plates were incubated overnight at

room temperature. The plates were again washed and a polyclonal rabbit anti-human IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum was added to each well. The plates were then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Jackson Labs.) was added at a 1:2000
5 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates were washed and TMB substrate added. The reaction was stopped after 20 min with 1 N sulfuric acid. Optical density was determined at 450 nm using 570 nm as a reference wavelength. Fractions that resulted in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone,
10 plus 3 standard deviations, were considered positive.

For sequencing, the polypeptides were individually dried onto Biobrene™ (Perkin Elmer/Applied BioSystems Division, Foster City, CA) treated glass fiber filters. The filters with polypeptide were loaded onto a Perkin Elmer/Applied BioSystems Division Procise 492 protein sequencer. The polypeptides were sequenced
15 from the amino terminal and using traditional Edman chemistry. The amino acid sequence was determined for each polypeptide by comparing the retention time of the PTH amino acid derivative to the appropriate PTH derivative standards.

Using the procedure described above, antigens having the following N-terminal sequences were isolated:

- 20 (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Xaa-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 54);
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 55);
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-
25 Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 56);
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 57);
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val (SEQ ID NO: 58);

- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 59);
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Ala-Ala-Ala-Ala-Pro-Pro-Ala (SEQ ID NO: 60); and
- 5 (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 61);

wherein Xaa may be any amino acid.

An additional antigen was isolated employing a microbore HPLC purification step in addition to the procedure described above. Specifically, 20 μ l of a
10 fraction comprising a mixture of antigens from the chromatographic purification step previously described, was purified on an Aquapore C18 column (Perkin Elmer/Applied Biosystems Division, Foster City, CA) with a 7 micron pore size, column size 1 mm x 100 mm, in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted from the column with a linear gradient of 1%/minute of acetonitrile
15 (containing 0.05% TFA) in water (0.05% TFA) at a flow rate of 80 μ l/minute. The eluent was monitored at 250 nm. The original fraction was separated into 4 major peaks plus other smaller components and a polypeptide was obtained which was shown to have a molecular weight of 12.054 Kd (by mass spectrometry) and the following N-terminal sequence:

- 20 (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Gln-Thr-Ser-Leu-Leu-Asn-Asn-Leu-Ala-Asp-Pro-Asp-Val-Ser-Phe-Ala-Asp (SEQ ID NO: 62).

This polypeptide was shown to induce proliferation and IFN- γ production in PBMC preparations using the assays described above.

25 Additional soluble antigens were isolated from *M. tuberculosis* culture filtrate as follows. *M. tuberculosis* culture filtrate was prepared as described above. Following dialysis against Bis-Tris propane buffer, at pH 5.5, fractionation was performed using anion exchange chromatography on a Poros QE column 4.6 x 100 mm (Perseptive Biosystems) equilibrated in Bis-Tris propane buffer pH 5.5. Polypeptides

were eluted with a linear 0-1.5 M NaCl gradient in the above buffer system at a flow rate of 10 ml/min. The column eluent was monitored at a wavelength of 214 nm.

The fractions eluting from the ion exchange column were pooled and subjected to reverse phase chromatography using a Poros R2 column 4.6 x 100 mm (Perseptive Biosystems). Polypeptides were eluted from the column with a linear gradient from 0-100% acetonitrile (0.1% TFA) at a flow rate of 5 ml/min. The eluent was monitored at 214 nm.

Fractions containing the eluted polypeptides were lyophilized and resuspended in 80 µl of aqueous 0.1% TFA and further subjected to reverse phase chromatography on a Vydac C4 column 4.6 x 150 mm (Western Analytical, Temecula, CA) with a linear gradient of 0-100% acetonitrile (0.1% TFA) at a flow rate of 2 ml/min. Eluent was monitored at 214 nm.

The fraction with biological activity was separated into one major peak plus other smaller components. Western blot of this peak onto PVDF membrane revealed three major bands of molecular weights 14 Kd, 20 Kd and 26 Kd. These polypeptides were determined to have the following N-terminal sequences, respectively:

(j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID NO: 129)

(k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID NO: 130) and

(l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID NO: 131), wherein Xaa may be any amino acid.

Using the assays described above, these polypeptides were shown to induce proliferation and IFN- γ production in PBMC preparations. Figs. 1A and B show the results of such assays using PBMC preparations from a first and a second donor, respectively.

DNA sequences that encode the antigens designated as (a), (c), (d) and (g) above were obtained by screening a *M. tuberculosis* genomic library using ³²P end labeled degenerate oligonucleotides corresponding to the N-terminal sequence and containing *M. tuberculosis* codon bias. The screen performed using a probe

corresponding to antigen (a) above identified a clone having the sequence provided in SEQ ID NO: 96. The polypeptide encoded by SEQ ID NO: 96 is provided in SEQ ID NO: 97. The screen performed using a probe corresponding to antigen (g) above identified a clone having the sequence provided in SEQ ID NO: 52. The polypeptide encoded by SEQ ID NO: 52 is provided in SEQ ID NO: 53. The screen performed using a probe corresponding to antigen (d) above identified a clone having the sequence provided in SEQ ID NO: 24, and the screen performed with a probe corresponding to antigen (c) identified a clone having the sequence provided in SEQ ID NO: 25.

The above amino acid sequences were compared to known amino acid sequences in the gene bank using the DNA STAR system. The database searched contains some 173,000 proteins and is a combination of the Swiss, PIR databases along with translated protein sequences (Version 87). No significant homologies to the amino acid sequences for antigens (a)-(h) and (l) were detected.

The amino acid sequence for antigen (i) was found to be homologous to a sequence from *M. leprae*. The full length *M. leprae* sequence was amplified from genomic DNA using the sequence obtained from GENBANK. This sequence was then used to screen an *M. tuberculosis* library and a full length copy of the *M. tuberculosis* homologue was obtained (SEQ ID NO: 94).

The amino acid sequence for antigen (j) was found to be homologous to a known *M. tuberculosis* protein translated from a DNA sequence. To the best of the inventors' knowledge, this protein has not been previously shown to possess T-cell stimulatory activity. The amino acid sequence for antigen (k) was found to be related to a sequence from *M. leprae*.

In the proliferation and IFN- γ assays described above, using three PPD positive donors, the results for representative antigens provided above are presented in Table 1:

TABLE 1
RESULTS OF PBMC PROLIFERATION AND IFN- γ ASSAYS

Sequence	Proliferation	IFN- γ
(a)	+	-
(c)	+++	+++
(d)	++	++
(g)	+++	+++
(h)	+++	+++

- 5 In Table 1, responses that gave a stimulation index (SI) of between 2 and 4 (compared to cells cultured in medium alone) were scored as +, as SI of 4-8 or 2-4 at a concentration of 1 μ g or less was scored as ++ and an SI of greater than 8 was scored as +++.
- 10 The antigen of sequence (i) was found to have a high SI (+++) for one donor and lower SI (++ and +) for the two other donors in both proliferation and IFN- γ assays.
- These results indicate that these antigens are capable of inducing proliferation and/or interferon- γ production.

EXAMPLE 2
USE OF PATIENT SERA TO ISOLATE *M. TUBERCULOSIS* ANTIGENS

15

This example illustrates the isolation of antigens from *M. tuberculosis* lysate by screening with serum from *M. tuberculosis*-infected individuals.

Dessicated *M. tuberculosis* H37Ra (Difco Laboratories) was added to a 2% NP40 solution, and alternately homogenized and sonicated three times. The resulting suspension was centrifuged at 13,000 rpm in microfuge tubes and the supernatant put through a 0.2 micron syringe filter. The filtrate was bound to Macro Prep DEAE beads (BioRad, Hercules, CA). The beads were extensively washed with 20 mM Tris pH 7.5 and bound proteins eluted with 1M NaCl. The NaCl elute was dialyzed overnight against 10 mM Tris, pH 7.5. Dialyzed solution was treated with

DNase and RNase at 0.05 mg/ml for 30 min. at room temperature and then with α -D-mannosidase, 0.5 U/mg at pH 4.5 for 3-4 hours at room temperature. After returning to pH 7.5, the material was fractionated via FPLC over a Bio Scale-Q-20 column (BioRad). Fractions were combined into nine pools, concentrated in a Centriprep 10 (Amicon, Beverley, MA) and screened by Western blot for serological activity using a serum pool from *M. tuberculosis*-infected patients which was not immunoreactive with other antigens of the present invention.

The most reactive fraction was run in SDS-PAGE and transferred to PVDF. A band at approximately 85 Kd was cut out yielding the sequence:

10 (m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132), wherein Xaa may be any amino acid.

Comparison of this sequence with those in the gene bank as described above, revealed no significant homologies to known sequences.

15 A DNA sequence that encodes the antigen designated as (m) above was obtained by screening a genomic *M. tuberculosis* Erdman strain library using labeled degenerate oligonucleotides corresponding to the N-terminal sequence of SEQ ID NO:137. A clone was identified having the DNA sequence provided in SEQ ID NO: 198. This sequence was found to encode the amino acid sequence provided in SEQ ID
20 NO: 199. Comparison of these sequences with those in the genebank revealed some similarity to sequences previously identified in *M. tuberculosis* and *M. bovis*.

EXAMPLE 3

PREPARATION OF DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

25

This example illustrates the preparation of DNA sequences encoding *M. tuberculosis* antigens by screening a *M. tuberculosis* expression library with sera obtained from patients infected with *M. tuberculosis*, or with anti-sera raised against *M. tuberculosis* antigens.

30

A. PREPARATION OF *M. TUBERCULOSIS* SOLUBLE ANTIGENS USING RABBIT ANTI-SERA RAISED AGAINST *M. TUBERCULOSIS* SUPERNATANT

Genomic DNA was isolated from the *M. tuberculosis* strain H37Ra. The DNA was randomly sheared and used to construct an expression library using the
5 Lambda ZAP expression system (Stratagene, La Jolla, CA). Rabbit anti-sera was generated against secretory proteins of the *M. tuberculosis* strains H37Ra, H37Rv and Erdman by immunizing a rabbit with concentrated supernatant of the *M. tuberculosis* cultures. Specifically, the rabbit was first immunized subcutaneously with 200 µg of protein antigen in a total volume of 2 ml containing 100 µg muramyl dipeptide
10 (Calbiochem, La Jolla, CA) and 1 ml of incomplete Freund's adjuvant. Four weeks later the rabbit was boosted subcutaneously with 100 µg antigen in incomplete Freund's adjuvant. Finally, the rabbit was immunized intravenously four weeks later with 50 µg protein antigen. The anti-sera were used to screen the expression library as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor
15 Laboratories, Cold Spring Harbor, NY, 1989. Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones deduced.

Thirty two clones were purified. Of these, 25 represent sequences that have not been previously identified in *M. tuberculosis*. Proteins were induced by IPTG
20 and purified by gel elution, as described in Skeiky et al., *J. Exp. Med.* 181:1527-1537, 1995. Representative partial sequences of DNA molecules identified in this screen are provided in SEQ ID NOS: 1-25. The corresponding predicted amino acid sequences are shown in SEQ ID NOS: 64-88.

On comparison of these sequences with known sequences in the gene
25 bank using the databases described above, it was found that the clones referred to hereinafter as TbRA2A, TbRA16, TbRA18, and TbRA29 (SEQ ID NOS: 77, 69, 71, 76) show some homology to sequences previously identified in *Mycobacterium leprae* but not in *M. tuberculosis*. TbRA2A was found to be a lipoprotein, with a six residue lipidation sequence being located adjacent to a hydrophobic secretory sequence.
30 TbRA11, TbRA26, TbRA28 and TbDPEP (SEQ ID NOS: 66, 74, 75, 53) have been

previously identified in *M. tuberculosis*. No significant homologies were found to TbRA1, TbRA3, TbRA4, TbRA9, TbRA10, TbRA13, TbRA17, TbRA19, TbRA29, TbRA32, TbRA36 and the overlapping clones TbRA35 and TbRA12 (SEQ ID NOS: 64, 78, 82, 83, 65, 68, 76, 72, 76, 79, 81, 80, 67, respectively). The clone
5 TbRa24 is overlapping with clone TbRa29.

B. USE OF SERA FROM PATIENTS HAVING PULMONARY OR PLEURAL TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

The genomic DNA library described above, and an additional H37Rv
10 library, were screened using pools of sera obtained from patients with active tuberculosis. To prepare the H37Rv library, *M. tuberculosis* strain H37Rv genomic DNA was isolated, subjected to partial Sau3A digestion and used to construct an expression library using the Lambda Zap expression system (Stratagene, La Jolla, Ca). Three different pools of sera, each containing sera obtained from three individuals with
15 active pulmonary or pleural disease, were used in the expression screening. The pools were designated TbL, TbM and TbH, referring to relative reactivity with H37Ra lysate (*i.e.*, TbL = low reactivity, TbM = medium reactivity and TbH = high reactivity) in both ELISA and immunoblot format. A fourth pool of sera from seven patients with active pulmonary tuberculosis was also employed. All of the sera lacked increased reactivity
20 with the recombinant 38 kD *M. tuberculosis* H37Ra phosphate-binding protein.

All pools were pre-adsorbed with *E. coli* lysate and used to screen the H37Ra and H37Rv expression libraries, as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. Bacteriophage plaques expressing immunoreactive antigens were purified.
25 Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones deduced.

Thirty two clones were purified. Of these, 31 represented sequences that had not been previously identified in human *M. tuberculosis*. Representative sequences of the DNA molecules identified are provided in SEQ ID NOS: 26-51 and 100. Of
30 these, TbH-8-2 (SEQ. ID NO. 100) is a partial clone of TbH-8, and TbH-4 (SEQ. ID

NO. 43) and TbH-4-FWD (SEQ. ID NO. 44) are non-contiguous sequences from the same clone. Amino acid sequences for the antigens hereinafter identified as Tb38-1, TbH-4, TbH-8, TbH-9, and TbH-12 are shown in SEQ ID NOS.: 89-93. Comparison of these sequences with known sequences in the gene bank using the databases
5 identified above revealed no significant homologies to TbH-4, TbH-8, TbH-9 and TbM-3, although weak homologies were found to TbH-9. TbH-12 was found to be homologous to a 34 kD antigenic protein previously identified in *M. paratuberculosis* (Acc. No. S28515). Tb38-1 was found to be located 34 base pairs upstream of the open reading frame for the antigen ESAT-6 previously identified in *M. bovis* (Acc.
10 No. U34848) and in *M. tuberculosis* (Sorensen et al., *Infect. Immun.* 63:1710-1717, 1995).

Probes derived from Tb38-1 and TbH-9, both isolated from an H37Ra library, were used to identify clones in an H37Rv library. Tb38-1 hybridized to Tb38-1F2, Tb38-1F3, Tb38-1F5 and Tb38-1F6 (SEQ. ID NOS: 107, 108, 111, 113, and
15 114). (SEQ ID NOS: 107 and 108 are non-contiguous sequences from clone Tb38-1F2.) Two open reading frames were deduced in Tb38-1F2; one corresponds to Tb37FL (SEQ. ID. NO. 109), the second, a partial sequence, may be the homologue of Tb38-1 and is called Tb38-IN (SEQ. ID NO. 110). The deduced amino acid sequence of Tb38-1F3 is presented in SEQ. ID. NO. 112. A TbH-9 probe identified three clones in the
20 H37Rv library: TbH-9-FL (SEQ. ID NO. 101), which may be the homologue of TbH-9 (R37Ra), TbH-9-1 (SEQ. ID NO. 103), and TbH-8-2 (SEQ. ID NO. 105) is a partial clone of TbH-8. The deduced amino acid sequences for these three clones are presented in SEQ ID NOS: 102, 104 and 106.

Further screening of the *M. tuberculosis* genomic DNA library, as
25 described above, resulted in the recovery of ten additional reactive clones, representing seven different genes. One of these genes was identified as the 38 Kd antigen discussed above, one was determined to be identical to the 14Kd alpha crystallin heat shock protein previously shown to be present in *M. tuberculosis*, and a third was determined to be identical to the antigen TbH-8 described above. The determined DNA sequences
30 for the remaining five clones (hereinafter referred to as TbH-29, TbH-30, TbH-32 and

TbH-33) are provided in SEQ ID NO: 133-136, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 137-140, respectively. The DNA and amino acid sequences for these antigens were compared with those in the gene bank as described above. No homologies were found to the 5' end of TbH-29 (which contains the reactive open reading frame), although the 3' end of TbH-29 was found to be identical to the *M. tuberculosis* cosmid Y227. TbH-32 and TbH-33 were found to be identical to the previously identified *M. tuberculosis* insertion element IS6110 and to the *M. tuberculosis* cosmid Y50, respectively. No significant homologies to TbH-30 were found.

Positive phagemid from this additional screening were used to infect *E. coli* XL-1 Blue MRF', as described in Sambrook et al., *supra*. Induction of recombinant protein was accomplished by the addition of IPTG. Induced and uninduced lysates were run in duplicate on SDS-PAGE and transferred to nitrocellulose filters. Filters were reacted with human *M. tuberculosis* sera (1:200 dilution) reactive with TbH and a rabbit sera (1:200 or 1:250 dilution) reactive with the N-terminal 4 Kd portion of lacZ. Sera incubations were performed for 2 hours at room temperature. Bound antibody was detected by addition of ¹²⁵I-labeled Protein A and subsequent exposure to film for variable times ranging from 16 hours to 11 days. The results of the immunoblots are summarized in Table 2.

TABLE 2

	<u>Antigen</u>	Human M. tb <u>Sera</u>	Anti-lacZ <u>Sera</u>
25	TbH-29	45 Kd	45 Kd
	TbH-30	No reactivity	29 Kd
	TbH-32	12 Kd	12 Kd
	TbH-33	16 Kd	16 Kd

Positive reaction of the recombinant human *M. tuberculosis* antigens with both the human *M. tuberculosis* sera and anti-lacZ sera indicate that reactivity of

the human *M. tuberculosis* sera is directed towards the fusion protein. Antigens reactive with the anti-lacZ sera but not with the human *M. tuberculosis* sera may be the result of the human *M. tuberculosis* sera recognizing conformational epitopes, or the antigen-antibody binding kinetics may be such that the 2 hour sera exposure in the immunoblot is not sufficient.

Studies were undertaken to determine whether the antigens TbH-9 and Tb38-1 represent cellular proteins or are secreted into *M. tuberculosis* culture media. In the first study, rabbit sera were raised against A) secretory proteins of *M. tuberculosis*, B) the known secretory recombinant *M. tuberculosis* antigen 85b, C) recombinant Tb38-1 and D) recombinant TbH-9, using protocols substantially as described in Example 3A. Total *M. tuberculosis* lysate, concentrated supernatant of *M. tuberculosis* cultures and the recombinant antigens 85b, TbH-9 and Tb38-1 were resolved on denaturing gels, immobilized on nitrocellulose membranes and duplicate blots were probed using the rabbit sera described above.

The results of this analysis using control sera (panel I) and antisera (panel II) against secretory proteins, recombinant 85b, recombinant Tb38-1 and recombinant TbH-9 are shown in Figures 2A-D, respectively, wherein the lane designations are as follows: 1) molecular weight protein standards; 2) 5 μ g of *M. tuberculosis* lysate; 3) 5 μ g secretory proteins; 4) 50 ng recombinant Tb38-1; 5) 50 ng recombinant TbH-9; and 6) 50 ng recombinant 85b. The recombinant antigens were engineered with six terminal histidine residues and would therefore be expected to migrate with a mobility approximately 1 kD larger than the native protein. In Figure 2D, recombinant TbH-9 is lacking approximately 10 kD of the full-length 42 kD antigen, hence the significant difference in the size of the immunoreactive native TbH-9 antigen in the lysate lane (indicated by an arrow). These results demonstrate that Tb38-1 and TbH-9 are intracellular antigens and are not actively secreted by *M. tuberculosis*.

The finding that TbH-9 is an intracellular antigen was confirmed by determining the reactivity of TbH-9-specific human T cell clones to recombinant TbH-9, secretory *M. tuberculosis* proteins and PPD. A TbH-9-specific T cell clone (designated 131TbH-9) was generated from PBMC of a healthy PPD-positive donor.

The proliferative response of 131TbH-9 to secretory proteins, recombinant TbH-9 and a control *M. tuberculosis* antigen, TbRa11, was determined by measuring uptake of tritiated thymidine, as described in Example 1. As shown in Figure 3A, the clone 131TbH-9 responds specifically to TbH-9, showing that TbH-9 is not a significant component of *M. tuberculosis* secretory proteins. Figure 3B shows the production of IFN- γ by a second TbH-9-specific T cell clone (designated PPD 800-10) prepared from PBMC from a healthy PPD-positive donor, following stimulation of the T cell clone with secretory proteins, PPD or recombinant TbH-9. These results further confirm that TbH-9 is not secreted by *M. tuberculosis*.

C. USE OF SERA FROM PATIENTS HAVING EXTRAPULMONARY TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda ZAP expression system (Stratagene, La Jolla, CA). The resulting library was screened using pools of sera obtained from individuals with extrapulmonary tuberculosis, as described above in Example 3B, with the secondary antibody being goat anti-human IgG + A + M (H+L) conjugated with alkaline phosphatase.

Eighteen clones were purified. Of these, 4 clones (hereinafter referred to as XP14, XP24, XP31 and XP32) were found to bear some similarity to known sequences. The determined DNA sequences for XP14, XP24 and XP31 are provided in SEQ ID NOS: 151-153, respectively, with the 5' and 3' DNA sequences for XP32 being provided in SEQ ID NOS: 154 and 155, respectively. The predicted amino acid sequence for XP14 is provided in SEQ ID NO: 156. The reverse complement of XP14 was found to encode the amino acid sequence provided in SEQ ID NO: 157.

Comparison of the sequences for the remaining 14 clones (hereinafter referred to as XP1-XP6, XP17-XP19, XP22, XP25, XP27, XP30 and XP36) with those in the genebank as described above, revealed no homologies with the exception of the 3' ends of XP2 and XP6 which were found to bear some homology to known *M. tuberculosis* cosmid. The DNA sequences for XP27 and XP36 are shown in SEQ ID

NOS: 158 and 159, respectively, with the 5' sequences for XP4, XP5, XP17 and XP30 being shown in SEQ ID NOS: 160-163, respectively, and the 5' and 3' sequences for XP2, XP3, XP6, XP18, XP19, XP22 and XP25 being shown in SEQ ID NOS: 164 and 165; 166 and 167; 168 and 169; 170 and 171; 172 and 173; 174 and 175; and 176 and 177, respectively. XP1 was found to overlap with the DNA sequences for TbH4, disclosed above. The full-length DNA sequence for TbH4-XP1 is provided in SEQ ID NO: 178. This DNA sequence was found to contain an open reading frame encoding the amino acid sequence shown in SEQ ID NO: 179. The reverse complement of TbH4-XP1 was found to contain an open reading frame encoding the amino acid sequence shown in SEQ ID NO: 180. The DNA sequence for XP36 was found to contain two open reading frames encoding the amino acid sequence shown in SEQ ID NOS: 181 and 182, with the reverse complement containing an open reading frame encoding the amino acid sequence shown in SEQ ID NO: 183.

Recombinant XP1 protein was prepared as described above in Example 3B, with a metal ion affinity chromatography column being employed for purification. Recombinant XP1 was found to stimulate cell proliferation and IFN- γ production in T cells isolated from an *M. tuberculosis*-immune donors.

D. USE OF A LYSATE POSITIVE SERUM POOL FROM PATIENTS HAVING TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda Screen expression system (Novagen, Madison, WI), as described below in Example 6. Pooled serum obtained from *M. tuberculosis*-infected patients and that was shown to react with *M. tuberculosis* lysate but not with the previously expressed proteins 38kD, Tb38-1, TbRa3, TbH4, DPEP and TbRa11, was used to screen the expression library as described above in Example 3B, with the secondary antibody being goat anti-human IgG + A + M (H+L) conjugated with alkaline phosphatase.

Twenty-seven clones were purified. Comparison of the determined cDNA sequences for these clones revealed no significant homologies to 10 of the clones

(hereinafter referred to as LSER-10, LSER-11, LSER-12, LSER-13, LSER-16, LSER-18, LSER-23, LSER-24, LSER-25 and LSER-27). The determined 5' cDNA sequences for LSER-10, LSER-11, LSER-12, LSER-13, LSER-16 and LSER-25 are provided in SEQ ID NO: 237-242, respectively, with the corresponding predicted amino acid sequences for LSER-10, LSER-12, LSER-13, LSER-16 and LSER-25 being provided in SEQ ID NO: 243-247, respectively. The determined full-length cDNA sequences for LSER-18, LSER-23, LSER-24 and LSER-27 are shown in SEQ ID NO: 248-251, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 252-255. The remaining seventeen clones were found to show similarities to unknown sequences previously identified in *M. tuberculosis*. The determined 5' cDNA sequences for sixteen of these clones (hereinafter referred to as LSER-1, LSER-3, LSER-4, LSER-5, LSER-6, LSER-8, LSER-14, LSER-15, LSER-17, LSER-19, LSER-20, LSER-22, LSER-26, LSER-28, LSER-29 and LSER-30) are provided in SEQ ID NO: 256-271, respectively, with the corresponding predicted amino acid sequences for LSER-1, LSER-3, LSER-5, LSER-6, LSER-8, LSER-14, LSER-15, LSER-17, LSER-19, LSER-20, LSER-22, LSER-26, LSER-28, LSER-29 and LSER-30 being provided in SEQ ID NO: 272-286, respectively. The determined full-length cDNA sequence for the clone LSER-9 is provided in SEQ ID NO: 287. The reverse complement of LSER-6 (SEQ ID NO: 288) was found to encode the predicted amino acid sequence of SEQ ID NO: 289.

E. PREPARATION OF *M. TUBERCULOSIS* SOLUBLE ANTIGENS USING RABBIT ANTISERA RAISED AGAINST *M. TUBERCULOSIS* FRACTIONATED PROTEINS

M. tuberculosis lysate was prepared as described above in Example 2. The resulting material was fractionated by HPLC and the fractions screened by Western blot for serological activity with a serum pool from *M. tuberculosis*-infected patients which showed little or no immunoreactivity with other antigens of the present invention. Rabbit anti-sera was generated against the most reactive fraction using the method described in Example 3A. The anti-sera was used to screen an *M. tuberculosis* Erdman strain genomic DNA expression library prepared as described above.

Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones determined.

Ten different clones were purified. Of these, one was found to be TbRa35, described above, and one was found to be the previously identified *M. tuberculosis* antigen, HSP60. Of the remaining eight clones, six (hereinafter referred to as RDIF2, RDIF5, RDIF8, RDIF10, RDIF11 and RDIF12) were found to bear some similarity to previously identified *M. tuberculosis* sequences. The determined DNA sequences for RDIF2, RDIF5, RDIF8, RDIF10 and RDIF11 are provided in SEQ ID NOS: 184-188, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NOS: 189-193, respectively. The 5' and 3' DNA sequences for RDIF12 are provided in SEQ ID NOS: 194 and 195, respectively. No significant homologies were found to the antigen RDIF-7. The determined DNA and predicted amino acid sequences for RDIF7 are provided in SEQ ID NOS: 196 and 197, respectively. One additional clone, referred to as RDIF6 was isolated, however, this was found to be identical to RDIF5.

Recombinant RDIF6, RDIF8, RDIF10 and RDIF11 were prepared as described above. These antigens were found to stimulate cell proliferation and IFN- γ production in T cells isolated from *M. tuberculosis*-immune donors.

EXAMPLE 4

PURIFICATION AND CHARACTERIZATION OF A POLYPEPTIDE FROM TUBERCULIN PURIFIED PROTEIN DERIVATIVE

An *M. tuberculosis* polypeptide was isolated from tuberculin purified protein derivative (PPD) as follows.

PPD was prepared as published with some modification (Seibert, F. et al., Tuberculin purified protein derivative. Preparation and analyses of a large quantity for standard. The American Review of Tuberculosis 44:9-25, 1941). *M. tuberculosis*

Rv strain was grown for 6 weeks in synthetic medium in roller bottles at 37°C. Bottles containing the bacterial growth were then heated to 100°C in water vapor for 3 hours. Cultures were sterile filtered using a 0.22 μ filter and the liquid phase was concentrated 20 times using a 3 kD cut-off membrane. Proteins were precipitated once with 50% ammonium sulfate solution and eight times with 25% ammonium sulfate solution. The resulting proteins (PPD) were fractionated by reverse phase liquid chromatography (RP-HPLC) using a C18 column (7.8 x 300 mM; Waters, Milford, MA) in a Biocad HPLC system (Perseptive Biosystems, Framingham, MA). Fractions were eluted from the column with a linear gradient from 0-100% buffer (0.1% TFA in acetonitrile). The flow rate was 10 ml/minute and eluent was monitored at 214 nm and 280 nm.

Six fractions were collected, dried, suspended in PBS and tested individually in *M. tuberculosis*-infected guinea pigs for induction of delayed type hypersensitivity (DTH) reaction. One fraction was found to induce a strong DTH reaction and was subsequently fractionated further by RP-HPLC on a microbore Vydac C18 column (Cat. No. 218TP5115) in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted with a linear gradient from 5-100% buffer (0.05% TFA in acetonitrile) with a flow rate of 80 μ l/minute. Eluent was monitored at 215 nm. Eight fractions were collected and tested for induction of DTH in *M. tuberculosis*-infected guinea pigs. One fraction was found to induce strong DTH of about 16 mm induration. The other fractions did not induce detectable DTH. The positive fraction was submitted to SDS-PAGE gel electrophoresis and found to contain a single protein band of approximately 12 kD molecular weight.

This polypeptide, herein after referred to as DPPD, was sequenced from the amino terminal using a Perkin Elmer/Applied Biosystems Division Procise 492 protein sequencer as described above and found to have the N-terminal sequence shown in SEQ ID NO: 124. Comparison of this sequence with known sequences in the gene bank as described above revealed no known homologies. Four cyanogen bromide fragments of DPPD were isolated and found to have the sequences shown in SEQ ID NOS: 125-128. A subsequent search of the *M. tuberculosis* genome database released by the Institute for Genomic Research revealed a match of the DPPD partial amino acid

sequence with a sequence present within the *M. tuberculosis* cosmid MTY21C12. An open reading frame of 336 bp was identified. The full-length DNA sequence for DPPD is provided in SEQ ID NO: 235, with the corresponding full-length amino acid sequence being provided in SEQ ID NO: 236.

5

EXAMPLE 5

USE OF SERA FROM TUBERCULOSIS-INFECTED MONKEYS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

10

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda ZAP expression system (Stratagene, La Jolla, CA). Serum samples were obtained from a cynomolgous monkey 18, 33, 51 and 56 days following infection with *M. tuberculosis* Erdman strain. These samples were pooled and used to screen the *M. tuberculosis* genomic DNA expression library using the procedure described above in Example 3C.

Twenty clones were purified. The determined 5' DNA sequences for the clones referred to as MO-1, MO-2, MO-4, MO-8, MO-9, MO-26, MO-28, MO-29, MO-30, MO-34 and MO-35 are provided in SEQ ID NO: 210-220, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 221-231. The full-length DNA sequence of the clone MO-10 is provided in SEQ ID NO: 232, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 233. The 3' DNA sequence for the clone MO-27 is provided in SEQ ID NO: 234.

Clones MO-1, MO-30 and MO-35 were found to show a high degree of relatedness and showed some homology to a previously identified unknown *M. tuberculosis* sequence and to cosmid MTCL237. MO-2 was found to show some homology to aspartokinase from *M. tuberculosis*. Clones MO-3, MO-7 and MO-27 were found to be identical and to show a high degree of relatedness to MO-5. All four of these clones showed some homology to *M. tuberculosis* heat shock protein 70. MO-27 was found to show some homology to *M. tuberculosis* cosmid MTCY339. MO-4

and MO-34 were found to show some homology to cosmid SCY21B4 and *M. smegmatis* integration host factor, and were both found to show some homology to a previously identified, unknown *M. tuberculosis* sequence. MO-6 was found to show some homology to *M. tuberculosis* heat shock protein 65. MO-8, MO-9, MO-10, MO-
5 26 and MO-29 were found to be highly related to each other and to show some homology to *M. tuberculosis* dihydrolipamide succinyltransferase. MO-28, MO-31 and MO-32 were found to be identical and to show some homology to a previously identified *M. tuberculosis* protein. MO-33 was found to show some homology to a previously identified 14 kDa *M. tuberculosis* heat shock protein.

10 Further studies using the above protocol resulted in the isolation of an additional four clones, hereinafter referred to as MO-12, MO-13, MO-19 and MO-39. The determined 5' cDNA sequences for these clones are provided in SEQ ID NO: 290-293, respectively, with the corresponding predicted protein sequences being provided in SEQ ID NO: 294-297, respectively. Comparison of these sequences with those in the
15 gene bank as described above revealed no significant homologies to MO-39. MO-12, MO-13 and MO-19 were found to show some homologies to unknown sequences previously isolated from *M. tuberculosis*.

EXAMPLE 6

20 ISOLATION OF DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS BY SCREENING OF A NOVEL EXPRESSION LIBRARY

This example illustrates isolation of DNA sequences encoding *M. tuberculosis* antigens by screening of a novel expression library with sera from *M.*
25 *tuberculosis*-infected patients that were shown to be unreactive with a panel of the recombinant *M. tuberculosis* antigens TbRa11, TbRa3, Tb38-1, TbH4, TbF and 38 kD.

Genomic DNA from *M. tuberculosis* Erdman strain was randomly sheared to an average size of 2 kb, and blunt ended with Klenow polymerase, followed by the addition of EcoRI adaptors. The insert was subsequently ligated into the Screen
30 phage vector (Novagen, Madison, WI) and packaged *in vitro* using the PhageMaker

extract (Novagen). The resulting library was screened with sera from several *M. tuberculosis* donors that had been shown to be negative on a panel of previously identified *M. tuberculosis* antigens as described above in Example 3B.

A total of 22 different clones were isolated. By comparison, screening of the λ Zap library described above using the same sera did not result in any positive hits. One of the clones was found to represent TbRa11, described above. The determined 5' cDNA sequences for 19 of the remaining 21 clones (hereinafter referred to as Erdsn1, Erdsn2, Erdsn4-Erdsn10, Erdsn12-18, Erdsn21-Erdsn23 and Erdsn25) are provided in SEQ ID NO: 298-317, respectively, with the determined 3' cDNA sequences for Erdsn1, Erdsn2, Erdsn4, Erdsn5, Erdsn7-Erdsn10, Erdsn12-Erdsn18, Erdsn21-Erdsn23 and Erdsn25 being provided in SEQ ID NO: 318-336, respectively. The complete cDNA insert sequence for the clone Erdsn24 is provided in SEQ ID NO: 337. Comparison of the determined cDNA sequences with those in the gene bank revealed no significant homologies to the sequences provided in SEQ ID NO: 304, 311, 313-315, 317, 319, 324, 326, 329, 331, 333, 335 and 337. The sequences of SEQ ID NO: 298-303, 305-310, 312, 316, 318, 320-321, 324-326, 328, 330, 332, 334 and 336 were found to show some homology to unknown sequences previously identified in *M. tuberculosis*.

20

EXAMPLE 7

ISOLATION OF SOLUBLE *M. TUBERCULOSIS* ANTIGENS

USING MASS SPECTROMETRY

This example illustrates the use of mass spectrometry to identify soluble *M. tuberculosis* antigens.

In a first approach, *M. tuberculosis* culture filtrate was screened by Western analysis using serum from a tuberculosis-infected individual. The reactive bands were excised from a silver stained gel and the amino acid sequences determined by mass spectrometry. The determined amino acid sequence for one of the isolated antigens is provided in SEQ ID NO: 338. Comparison of this sequence with those in

the gene bank revealed homology to the 85b precursor antigen previously identified in *M. tuberculosis*.

In a second approach, the high molecular weight region of *M. tuberculosis* culture supernatant was studied. This area may contain immunodominant antigens which may be useful in the diagnosis of *M. tuberculosis* infection. Two known monoclonal antibodies, IT42 and IT57 (available from the Center for Disease Control, Atlanta, GA), show reactivity by Western analysis to antigens in this vicinity, although the identity of the antigens remains unknown. In addition, unknown high-molecular weight proteins have been described as containing a surrogate marker for *M. tuberculosis* infection in HIV-positive individuals (*Jnl. Infect. Dis.*, 176:133-143, 1997). To determine the identity of these antigens, two-dimensional gel electrophoresis and two-dimensional Western analysis were performed using the antibodies IT57 and IT42. Five protein spots in the high molecular weight region were identified, individually excised, enzymatically digested and subjected to mass spectrometric analysis.

The determined amino acid sequences for three of these spots (referred to as spots 1, 2 and 4) are provided in SEQ ID NO: 339, 340-341 and 342, respectively. Comparison of these sequences with those in the gene bank revealed that spot 1 is the previously identified PcK-1, a phosphoenolpyruvate kinase. The two sequences isolated from spot 2 were determined to be from two DNAs, previously identified in *M. tuberculosis* as heat shock proteins. Spot 4 was determined to be the previously identified *M. tuberculosis* protein Kat G. To the best of the inventors' knowledge, neither PcK-1 nor the two DNAs have previously been shown to have utility in the diagnosis of *M. tuberculosis* infection.

EXAMPLE 8

SYNTHESIS OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be

attached to the amino terminus of the peptide to provide a method of conjugation or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

This procedure was used to synthesize a TbM-1 peptide that contains one and a half repeats of a TbM-1 sequence. The TbM-1 peptide has the sequence GCGDRSGGNLDQIRLRDRSGGNL (SEQ ID NO: 63).

15

EXAMPLE 9

USE OF REPRESENTATIVE ANTIGENS FOR SERODIAGNOSIS OF TUBERCULOSIS

This Example illustrates the diagnostic properties of several representative antigens.

Assays were performed in 96-well plates were coated with 200 ng antigen diluted to 50 μ L in carbonate coating buffer, pH 9.6. The wells were coated overnight at 4°C (or 2 hours at 37°C). The plate contents were then removed and the wells were blocked for 2 hours with 200 μ L of PBS/1% BSA. After the blocking step, the wells were washed five times with PBS/0.1% Tween 20™. 50 μ L sera, diluted 1:100 in PBS/0.1% Tween 20™/0.1% BSA, was then added to each well and incubated for 30 minutes at room temperature. The plates were then washed again five times with PBS/0.1% Tween 20™.

The enzyme conjugate (horseradish peroxidase - Protein A, Zymed, San Francisco, CA) was then diluted 1:10,000 in PBS/0.1% Tween 20™/0.1% BSA, and 50

μ L of the diluted conjugate was added to each well and incubated for 30 minutes at room temperature. Following incubation, the wells were washed five times with PBS/0.1% Tween 20™. 100 μ L of tetramethylbenzidine peroxidase (TMB) substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) was added, undiluted, and
5 incubated for about 15 minutes. The reaction was stopped with the addition of 100 μ L of 1 N H_2SO_4 to each well, and the plates were read at 450 nm.

Figure 4 shows the ELISA reactivity of two recombinant antigens isolated using method A in Example 3 (TbRa3 and TbRa9) with sera from *M. tuberculosis* positive and negative patients. The reactivity of these antigens is
10 compared to that of bacterial lysate isolated from *M. tuberculosis* strain H37Ra (Difco, Detroit, MI). In both cases, the recombinant antigens differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 56 out of 87 positive sera, and TbRa9 detected 111 out of 165 positive sera.

Figure 5 illustrates the ELISA reactivity of representative antigens
15 isolated using method B of Example 3. The reactivity of the recombinant antigens TbH4, TbH12, Tb38-1 and the peptide TbM-1 (as described in Example 4) is compared to that of the 38 kD antigen described by Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989. Again, all of the polypeptides tested differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbH4
20 detected 67 out of 126 positive sera, TbH12 detected 50 out of 125 positive sera, 38-1 detected 61 out of 101 positive sera and the TbM-1 peptide detected 25 out of 30 positive sera.

The reactivity of four antigens (TbRa3, TbRa9, TbH4 and TbH12) with sera from a group of *M. tuberculosis* infected patients with differing reactivity in the
25 acid fast stain of sputum (Smithwick and David, *Tubercle* 52:226, 1971) was also examined, and compared to the reactivity of *M. tuberculosis* lysate and the 38 kD antigen. The results are presented in Table 3, below:

TABLE 3

REACTIVITY OF ANTIGENS WITH SERA FROM *M. TUBERCULOSIS* PATIENTS

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-2	++++	1.853	0.634	0.998	1.022	1.030	1.314
Tb01B93I-19	++++	2.657	2.322	0.608	0.837	1.857	2.335
Tb01B93I-8	+++	2.703	0.527	0.492	0.281	0.501	2.002
Tb01B93I-10	++	1.665	1.301	0.685	0.216	0.448	0.458
Tb01B93I-11	+++	2.817	0.697	0.509	0.301	0.173	2.608
Tb01B93I-15	+++	1.28	0.283	0.808	0.218	1.537	0.811
Tb01B93I-16	+++	2.908	>3	0.899	0.441	0.593	1.080
Tb01B93I-25	—	0.395	0.131	0.335	0.211	0.107	0.948
Tb01B93I-87	+++	2.653	2.432	2.282	0.977	1.221	0.857
Tb01B93I-89	—	1.912	2.370	2.436	0.876	0.520	0.952
Tb01B94I-108	—	1.639	0.341	0.797	0.368	0.654	0.798
Tb01B94I-201	—	1.721	0.419	0.661	0.137	0.064	0.692
Tb01B93I-88	—	1.939	1.269	2.519	1.381	0.214	0.530
Tb01B93I-92	—	2.355	2.329	2.78	0.685	0.997	2.527
Tb01B94I-109	++	0.993	0.620	0.574	0.441	0.5	2.558
Tb01B94I-210	++	2.777	>3	0.393	0.367	1.004	1.315
Tb01B94I-224	—	2.913	0.476	0.251	1.297	1.990	0.256
Tb01B93I-9	+	2.649	0.278	0.210	0.140	0.181	1.586
Tb01B93I-14	+	>3	1.538	0.282	0.291	0.549	2.880
Tb01B93I-21	+	2.645	0.739	2.499	0.783	0.536	1.770

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-22	+	0.714	0.451	2.082	0.285	0.269	1.159
Tb01B93I-31	+	0.956	0.490	1.019	0.812	0.176	1.293
Tb01B93I-32	-	2.261	0.786	0.668	0.273	0.535	0.405
Tb01B93I-52	-	0.658	0.114	0.434	0.330	0.273	1.140
Tb01B93I-99	-	2.118	0.584	1.62	0.119	0.977	0.729
Tb01B94I-130	-	1.349	0.224	0.86	0.282	0.383	2.146
Tb01B94I-131	-	0.685	0.324	1.173	0.059	0.118	1.431
AT4-0070	Normal	0.072	0.043	0.092	0.071	0.040	0.039
AT4-0105	Normal	0.397	0.121	0.118	0.103	0.078	0.390
3/15/94-1	Normal	0.227	0.064	0.098	0.026	0.001	0.228
4/15/93-2	Normal	0.114	0.240	0.071	0.034	0.041	0.264
5/26/94-4	Normal	0.089	0.259	0.096	0.046	0.008	0.053
5/26/94-3	Normal	0.139	0.093	0.085	0.019	0.067	0.01

Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 23 out of 27 positive sera, TbRa9 detected 22 out of 27, TbH4 detected 18 out of 27 and TbH12 detected 15 out of 27. If used in combination, these four antigens would have a theoretical sensitivity of 27 out of 27, indicating that these antigens should complement each other in the serological detection of *M. tuberculosis* infection. In addition, several of the recombinant antigens detected positive sera that were not detected using the 38 kD antigen, indicating that these antigens may be complementary to the 38 kD antigen.

The reactivity of the recombinant antigen TbRa11 with sera from *M. tuberculosis* patients shown to be negative for the 38 kD antigen, as well as with sera from PPD positive and normal donors, was determined by ELISA as described above.

The results are shown in Figure 6 which indicates that TbRa11, while being negative with sera from PPD positive and normal donors, detected sera that were negative with the 38 kD antigen. Of the thirteen 38 kD negative sera tested, nine were positive with TbRa11, indicating that this antigen may be reacting with a sub-group of 38 kD antigen negative sera. In contrast, in a group of 38 kD positive sera where TbRa11 was reactive, the mean OD 450 for TbRa11 was lower than that for the 38 kD antigen. The data indicate an inverse relationship between the presence of TbRa11 activity and 38 kD positivity.

The antigen TbRa2A was tested in an indirect ELISA using initially 50 μ l of serum at 1:100 dilution for 30 minutes at room temperature followed by washing in PBS Tween and incubating for 30 minutes with biotinylated Protein A (Zymed, San Francisco, CA) at a 1:10,000 dilution. Following washing, 50 μ l of streptavidin-horseradish peroxidase (Zymed) at 1:10,000 dilution was added and the mixture incubated for 30 minutes. After washing, the assay was developed with TMB substrate as described above. The reactivity of TbRa2A with sera from *M. tuberculosis* patients and normal donors is shown in Table 4. The mean value for reactivity of TbRa2A with sera from *M. tuberculosis* patients was 0.444 with a standard deviation of 0.309. The mean for reactivity with sera from normal donors was 0.109 with a standard deviation of 0.029. Testing of 38 kD negative sera (Figure 7) also indicated that the TbRa2A antigen was capable of detecting sera in this category.

TABLE 4
REACTIVITY OF TBRA2A WITH SERA FROM *M. TUBERCULOSIS* PATIENTS AND FROM
NORMAL DONORS

Serum ID	Status	OD 450
Tb85	TB	0.680
Tb86	TB	0.450
Tb87	TB	0.263
Tb88	TB	0.275
Tb89	TB	0.403
Tb91	TB	0.393
Tb92	TB	0.401

Tb93	TB	0.232
Tb94	TB	0.333
Tb95	TB	0.435
Tb96	TB	0.284
Tb97	TB	0.320
Tb99	TB	0.328
Tb100	TB	0.817
Tb101	TB	0.607
Tb102	TB	0.191
Tb103	TB	0.228
Tb107	TB	0.324
Tb109	TB	1.572
Tb112	TB	0.338
DL4-0176	Normal	0.036
AT4-0043	Normal	0.126
AT4-0044	Normal	0.130
AT4-0052	Normal	0.135
AT4-0053	Normal	0.133
AT4-0062	Normal	0.128
AT4-0070	Normal	0.088
AT4-0091	Normal	0.108
AT4-0100	Normal	0.106
AT4-0105	Normal	0.108
AT4-0109	Normal	0.105

The reactivity of the recombinant antigen (g) (SEQ ID NO: 60) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. Figure 8 shows the results of the titration of antigen (g) with four *M. tuberculosis* positive sera that were all reactive with the 38 kD antigen and with four donor sera. All four positive sera were reactive with antigen (g).

The reactivity of the recombinant antigen TbH-29 (SEQ ID NO: 137) with sera from *M. tuberculosis* patients, PPD positive donors and normal donors was determined by indirect ELISA as described above. The results are shown in Figure 9. TbH-29 detected 30 out of 60 *M. tuberculosis* sera, 2 out of 8 PPD positive sera and 2 out of 27 normal sera.

Figure 10 shows the results of ELISA tests (both direct and indirect) of the antigen TbH-33 (SEQ ID NO: 140) with sera from *M. tuberculosis* patients and from normal donors and with a pool of sera from *M. tuberculosis* patients. The mean

OD 450 was demonstrated to be higher with sera from *M. tuberculosis* patients than from normal donors, with the mean OD 450 being significantly higher in the indirect ELISA than in the direct ELISA. Figure 11 is a titration curve for the reactivity of recombinant TbH-33 with sera from *M. tuberculosis* patients and from normal donors showing an increase in OD 450 with increasing concentration of antigen.

The reactivity of the recombinant antigens RDIF6, RDIF8 and RDIF10 (SEQ ID NOS: 184-187, respectively) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. RDIF6 detected 6 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; RDIF8 detected 14 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; and RDIF10 detected 4 out of 27 *M. tuberculosis* sera and 1 out of 15 normal sera. In addition, RDIF10 was found to detect 0 out of 5 sera from PPD-positive donors.

The antigens MO-1, MO-2, MO-4, MO-28 and MO-29 described above in Example 5, were expressed in *E. coli* and purified using a hexahistidine tag. The reactivity of these antigens with both *M. tuberculosis* positive and negative sera was examined by ELISA as described above. Titration curves showing the reactivity of MO-1, MO-2, MO-4, MO-28 and MO-29 at different solid phase coat levels when tested against four *M. tuberculosis* positive sera and four *M. tuberculosis* negative sera are shown in Figs. 12A-E, respectively. Three of the clones, MO-1, MO-2 and MO-29 were further tested on panels of HIV positive/tuberculosis (HIV/TB) positive and extrapulmonary sera. MO-1 detected 3/20 extrapulmonary and 2/38 HIV/TB sera. On the same sera groups, MO-2 detected 2/20 and 10/38, and MO-29 detected 2/20 and 8/38 sera. In combination these three clones would have detected 4/20 extrapulmonary sera and 16/38 HIV/TB sera. In addition, MO-1 detected 6/17 sera that had previously been shown only to react with *M. tuberculosis* lysate and not with either 38 kD or with other antigens of the subject invention.

EXAMPLE 10

PREPARATION AND CHARACTERIZATION OF *M. TUBERCULOSIS* FUSION PROTEINS

5 A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR in order to facilitate their fusion and the subsequent expression of the fusion protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 141 and 142), PDM-57 and PDM-58 (SEQ ID NO: 143 and 144), and PDM-69 and PDM-60 (SEQ ID NO: 145-146), respectively. In each case, the DNA amplification was performed using 10 µl 10X Pfu buffer, 2 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 81.5 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at either 70 ng/µl (for TbRa3) or 50 ng/µl (for 38 kD and Tb38-1). For 15 TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15 sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°C for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for 1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by 20 72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned directly into pT7⁺L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and 25 then digested with EcoRI for direct cloning into the pT7⁺L2Ra3-1 vector which was digested with StuI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and EcoRI and directly subcloned into pT7⁺L2Ra3/38kD-17 digested with the same enzymes. The whole fusion was then transferred to pET28b using NdeI and EcoRI sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed to BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with the same antibiotics and the culture was induced with IPTG at an OD₅₆₀ of 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 26,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 147 and 148, respectively.

A fusion protein containing the two antigens TbH-9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 151.

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO:145 and PDM-83 (SEQ ID NO: 200) being used for amplification of the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a DraI site at the 3' end of the coding region that keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using NdeI and EcoRI sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and PDM-85 (SEQ ID NO: 201 and 202, respectively) and 1 µl DNA at 50 ng/µl.

Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with EcoRI and Eco72I and clones directly into the pET28Ra3/38kD/38-1A construct which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 203 and 204, respectively.

10 A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and TbH4 was prepared as follows.

Genomic *M. tuberculosis* DNA was used to PCR full-length TbH4 (FL TbH4) with the primers PDM-157 and PDM-160 (SEQ ID NO: 343 and 344, respectively) and 2 µl DNA at 100 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 61 °C for 20 sec and 72 °C for 5 min; and finally by annealing at 72 °C for 10 min. The FL TbH4 PCR fragment was digested with EcoRI and Sca I (New England Biolabs.) and cloned directly into the pET28Ra3/38kD/38-1A construct described above which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-6) are provided in SEQ ID NO: 345 and 346, respectively.

A fusion protein containing the antigen 38kD and DPEP separated by a linker was prepared as follows.

25 38 kD DNA was used to perform PCR using the primers PDM-176 and PDM-175 (SEQ ID NO: 347 and 348, respectively), and 1 µl PET28Ra3/38kD/38-1/Ra2A-12 DNA at 110 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 71 °C for 15 sec and 72 °C for 5 min and 40 sec; and finally by annealing at 72 °C for 4 min. The two sets of primers PDM-171, PDM-172, and PDM-173, PDM-174 were annealed by heating to 95 °C for 2 min and

30

then ramping down to 25 °C slowly at 0.1 °C/sec. DPEP DNA was used to perform PCR as described above. The 38 kD fragment was digested with Eco RI (New England Biolabs) and cloned into a modified pT7ΔL2 vector which was cut with Eco 72 I (Promega) and Eco RI. The modified pT7ΔL2 construct was designed to have a 5 MGHHHHHH amino acid coding region in frame just 5' of the Eco 72 I site. The construct was digested with Kpn 2I (Gibco, BRL) and Pst I (New England Biolabs) and the annealed sets of phosphorylated primers (PDM-171, PDM-172 and PDM-173, PDM-174) were cloned in. The DPEP PCR fragment was digested with Eco RI and Eco 72 I and cloned into this second construct which was digested with Eco 47 III (New England Biolabs) and Eco RI. Ligations were done with a ligation kit from Panvera (Madison, WI). The resulting construct was digested with NdeI (New England Biolabs) and Eco RI, and transferred to a modified pET28 vector. The fusion construct was confirmed to be correct by DNA sequencing.

Recombinant protein was prepared essentially as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-8) are provided in SEQ ID NO: 349 and 350, respectively.

EXAMPLE 11

USE OF *M. TUBERCULOSIS* FUSION PROTEINS FOR SERODIAGNOSIS OF TUBERCULOSIS

The effectiveness of the fusion protein TbRa3-38 kD-Tb38-1, prepared as described above, in the serodiagnosis of tuberculosis infection was examined by ELISA.

The ELISA protocol was as described above in Example 6, with the fusion protein being coated at 200 ng/well. A panel of sera was chosen from a group of tuberculosis patients previously shown, either by ELISA or by western blot analysis, to react with each of the three antigens individually or in combination. Such a panel enabled the dissection of the serological reactivity of the fusion protein to determine if

all three epitopes functioned with the fusion protein. As shown in Table 5, all four sera that reacted with TbRa3 only were detectable with the fusion protein. Three sera that reacted only with Tb38-1 were also detectable, as were two sera that reacted with 38 kD alone. The remaining 15 sera were all positive with the fusion protein based on a cut-off in the assay of mean negatives +3 standard deviations. This data demonstrates the functional activity of all three epitopes in the fusion protein.

TABLE 5
REACTIVITY OF TRI-PEPTIDE FUSION PROTEIN WITH SERA FROM *M. TUBERCULOSIS* PATIENTS

Serum ID	Status	ELISA and/or Western Blot Reactivity with Individual proteins			Fusion Recombinant OD 450	Fusion Recombinant Status
		38kd	Tb38-1	TbRa3		
01B93I-40	TB	-	-	+	0.413	+
01B93I-41	TB	-	+	+	0.392	+
01B93I-29	TB	+	-	+	2.217	+
01B93I-109	TB	+	±	+	0.522	+
01B93I-132	TB	+	+	-	0.937	+
5004	TB	=	-	=	1.098	+
15004	TB	-	-	+	2.077	+
39004	TB	+	±	-	1.675	+
68004	TB	-	+	+	2.388	+
99004	TB	-	+	±	0.607	+
107004	TB	-	-	=	0.667	+
92004	TB	+	±	±	1.070	+
97004	TB	+	-	=	1.152	+
118004	TB	+	-	=	2.694	+
173004	TB	+	+	+	3.258	+
175004	TB	+	-	+	2.514	+
274004	TB	-	-	+	3.220	+
276004	TB	-	+	-	2.991	+
282004	TB	+	-	-	0.824	+
289004	TB	-	-	+	0.848	+

308004	TB	-	+	-	3.338	+
314004	TB	-	+	-	1.362	+
317004	TB	+	-	-	0.763	+
312004	TB	-	-	+	1.079	+
D176	PPD	-	-	-	0.145	-
D162	PPD	-	-	-	0.073	-
D161	PPD	-	-	-	0.097	-
D27	PPD	-	-	-	0.082	-
A6-124	NORMAL	-	-	-	0.053	-
A6-125	NORMAL	-	-	-	0.087	-
A6-126	NORMAL	-	-	-	0.346	±
A6-127	NORMAL	-	-	-	0.064	-
A6-128	NORMAL	-	-	-	0.034	-
A6-129	NORMAL	-	-	-	0.037	-
A6-130	NORMAL	-	-	-	0.057	-
A6-131	NORMAL	-	-	-	0.054	-
A6-132	NORMAL	-	-	-	0.022	-
A6-133	NORMAL	-	-	-	0.147	-
A6-134	NORMAL	-	-	-	0.101	-
A6-135	NORMAL	-	-	-	0.066	-
A6-136	NORMAL	-	-	-	0.054	-
A6-137	NORMAL	-	-	-	0.065	-
A6-138	NORMAL	-	-	-	0.041	-
A6-139	NORMAL	-	-	-	0.103	-
A6-140	NORMAL	-	-	-	0.212	-
A6-141	NORMAL	-	-	-	0.056	-
A6-142	NORMAL	-	-	-	0.051	-

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 6) demonstrate that all four antigens function independently in the fusion protein.

TABLE 6
 REACTIVITY OF TbF-2 FUSION PROTEIN WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRa3	Tb38-l	DPEP
B931-40	TB	0.57	+	0.321	+	-	+	-	+
B931-41	TB	0.601	+	0.396	+	+	+	+	-
B931-109	TB	0.494	+	0.404	+	+	+	±	-
B931-132	TB	1.502	+	1.292	+	+	+	-	±
5004	TB	1.806	+	1.666	+	±	±	-	-
15004	TB	2.862	-	2.468	-	-	-	-	-
39004	TB	2.443	-	1.722	-	+	+	-	-
68004	TB	2.871	-	2.575	+	-	-	-	-
99004	TB	0.691	-	0.971	-	-	±	-	-
107004	TB	0.875	-	0.732	-	-	±	-	-
92004	TB	1.632	-	1.394	-	-	±	-	-
97004	TB	1.491	-	1.979	+	+	±	-	+
118004	TB	3.182	+	3.045	+	+	±	-	-
173004	TB	3.644	-	3.578	+	+	+	+	-
175004	TB	3.332	+	2.916	-	+	-	-	-
274004	TB	3.696	-	3.716	-	-	-	-	+
276004	TB	3.243	-	2.56	+	-	-	-	-
282004	TB	1.249	-	1.234	-	-	-	-	-
289004	TB	1.373	-	1.17	+	-	-	-	-
308004	TB	3.708	-	3.355	+	-	-	-	-
314004	TB	1.663	-	1.399	-	-	-	-	-
317004	TB	1.163	-	0.92	-	-	-	-	-
312004	TB	1.709	-	1.453	-	-	-	-	-
380004	TB	0.238	-	0.461	-	-	-	-	-
451004	TB	0.18	-	0.2	-	-	-	-	-
478004	TB	0.188	-	0.469	-	-	-	-	±
410004	TB	0.384	-	2.392	-	±	-	-	-
411004	TB	0.306	-	0.874	-	-	-	-	-
421004	TB	0.357	-	1.456	-	-	-	-	-
528004	TB	0.047	-	0.196	-	-	-	-	-
A6-87	Normal	0.094	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.125	-	-	-	-	-
A6-90	Normal	0.179	-	0.206	-	-	-	-	-
A6-91	Normal	0.135	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.097	-	-	-	-	-
A6-93	Normal	0.072	-	0.098	-	-	-	-	-
A6-94	Normal	0.072	-	0.064	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.121	-	0.12	-	-	-	-	-
Cut-off		0.284		0.266					

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the
5 construction of fusion proteins.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the
10 invention.

CLAIMS

We claim:

1. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 115);
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 116);
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 17);
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 118);
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val (SEQ ID NO: 119);
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 120);
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser (SEQ ID NO: 121);
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 122);
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn (SEQ ID NO: 123); and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID NO: 131)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID NO: 124) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132), wherein Xaa may be any amino acid.

3. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an antigenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. A recombinant expression vector comprising a DNA molecule according to claim 5.
7. A host cell transformed with an expression vector according to claim 6.
8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:
 - (a) contacting a biological sample with one or more polypeptides according to any of claims 1-4; and
 - (b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.
10. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:
 - (a) contacting a biological sample with a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and
 - (b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.
11. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:
 - (a) contacting a biological sample with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said

sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

12. The method of any one of claims 9-11 wherein step (a) additionally comprises contacting the biological sample with a 38 kD *M. tuberculosis* antigen and step (b) additionally comprises detecting in the sample the presence of antibodies that bind to the 38 kD *M. tuberculosis* antigen.

13. The method of any one of claims 9-11 wherein the polypeptide(s) are bound to a solid support.

14. The method of claim 13 wherein the solid support comprises nitrocellulose, latex or a plastic material.

15. The method of any one of claims 9-11 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

16. The method of claim 15 wherein the biological sample is whole blood or serum.

17. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

18. The method of claim 17, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule according to claim 5.

19. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

20. The method of claim 19, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

21. The method of claims 17 or 19 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

22. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

23. The method of claim 22 wherein the probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

24. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

25. The method of claim 24 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

26. The method of claims 22 or 24 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

27. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide according to any one of claims 1-4; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

28. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

29. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

30. The method of any one of claims 27-29 wherein the binding agent is a monoclonal antibody.

31. The method of any one of claims 27-29 wherein the binding agent is a polyclonal antibody.
32. A diagnostic kit comprising:
- (a) one or more polypeptides according to any of claims 1-4; and
 - (b) a detection reagent.
33. A diagnostic kit comprising:
- (a) one or more polypeptides having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and
 - (b) a detection reagent.
34. A diagnostic kit comprising:
- (a) one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and
 - (b) a detection reagent.
35. The kit of any one of claims 32-34 wherein the polypeptide(s) are immobilized on a solid support.
36. The kit of claim 35 wherein the solid support comprises nitrocellulose, latex or a plastic material.
37. The kit of any one of claims 32-34 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

38. The kit of claim 37 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

39. The kit of claim 37 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin, dye particles and colloidal particles.

40. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule according to claim 5.

41. A diagnostic kit according to claim 40, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA molecule according to claim 5.

42. A diagnostic kit comprising a at least two oligonucleotide primers, at least one of the primers being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

43. A diagnostic kit according to claim 42, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA molecule according to claim 5.

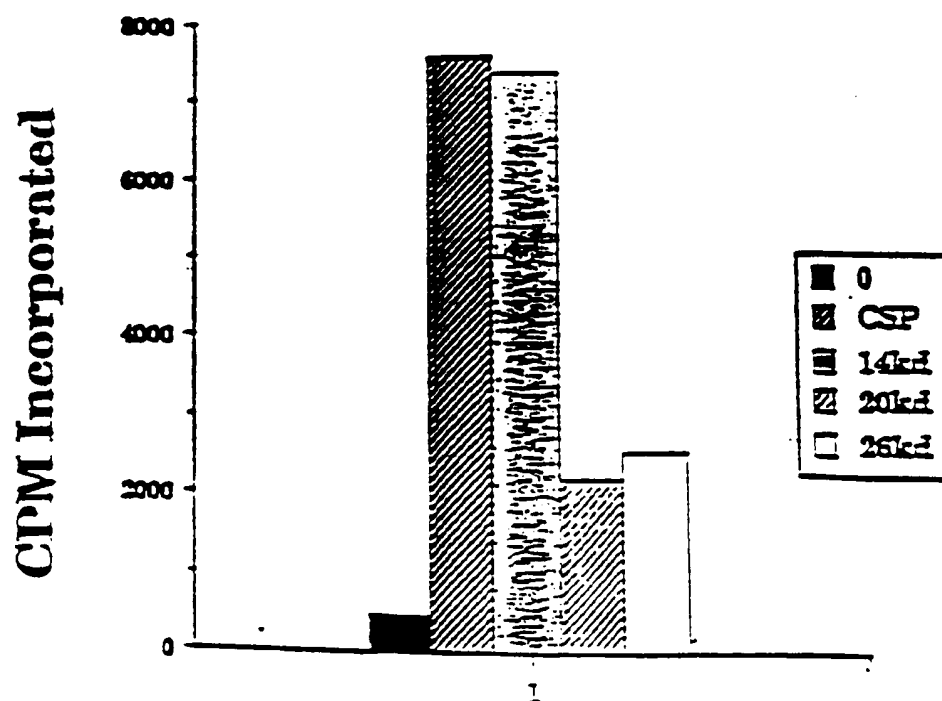
45. A kit according to claim 44, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.
46. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.
47. A kit according to claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.
48. A monoclonal antibody that binds to a polypeptide according to any of claims 1-4.
49. A polyclonal antibody that binds to a polypeptide according to any of claims 1-4.
50. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.
51. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6 (SEQ ID NO: 99).
52. A fusion protein comprising a polypeptide having an N-terminal sequence selected from the group of sequences provided in SEQ ID NOS: 129 and 130.

53. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO: 150).

54. A diagnostic kit comprising:

- (a) one or more fusion proteins according to any one of claims 50-53; and
- (b) a detection reagent.

D7 T Cell Proliferation



D7 IFN_γ

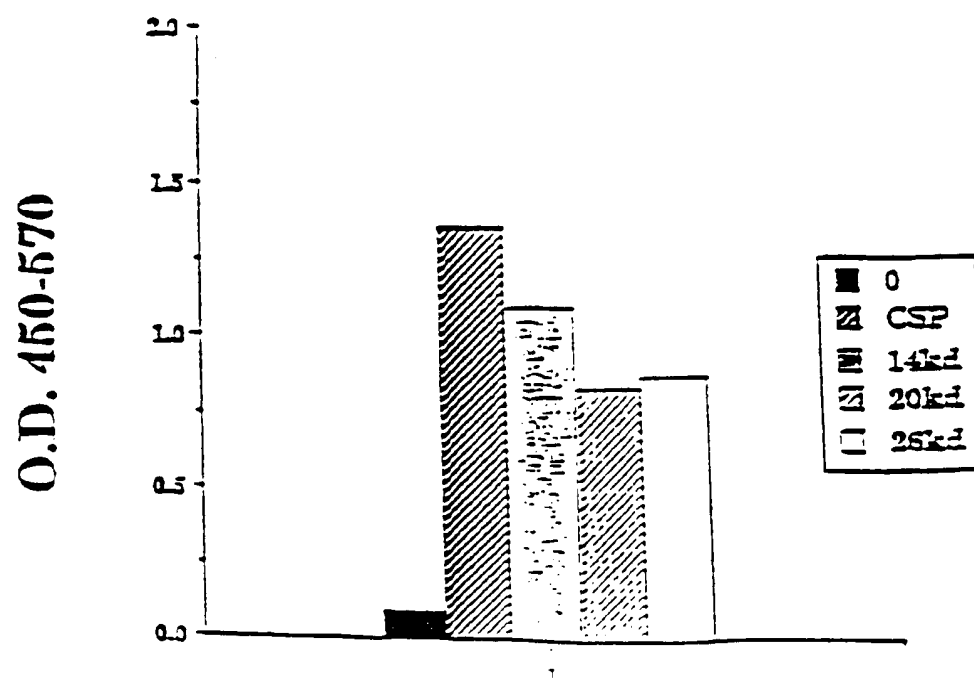
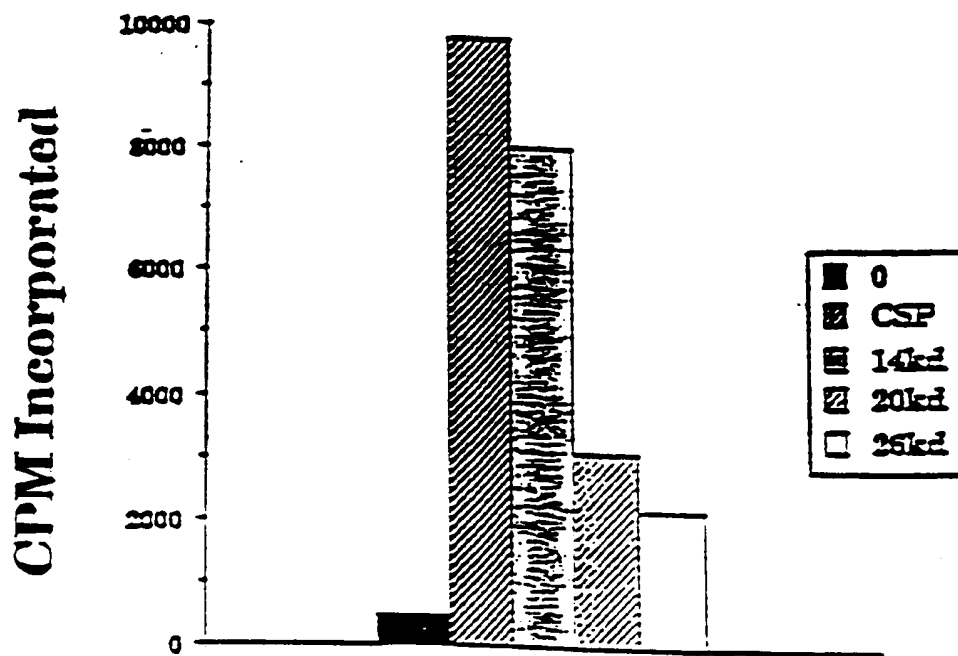


FIG. 1A

D160 T Cell Proliferation



D160 IFN γ

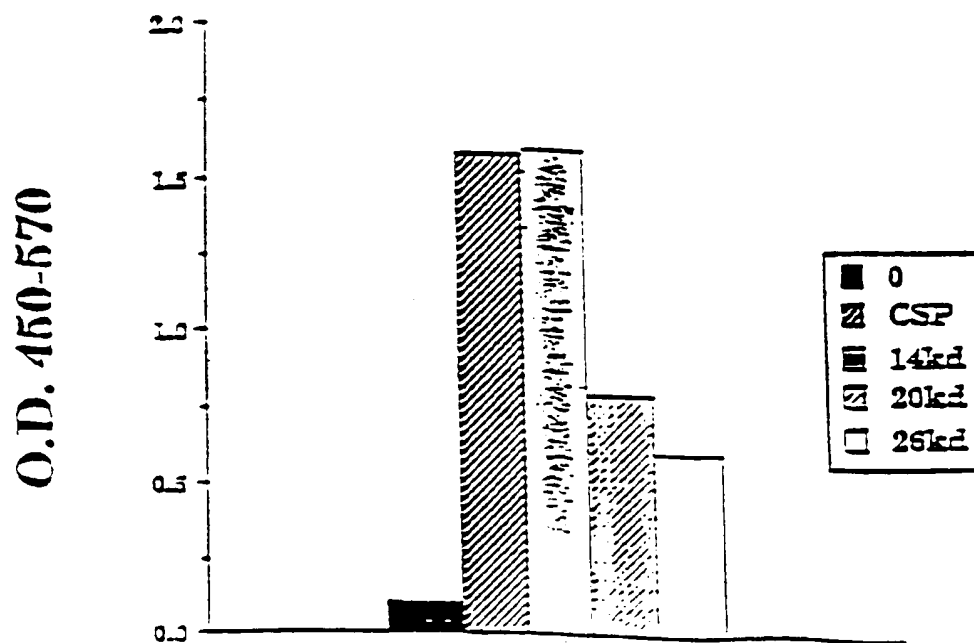
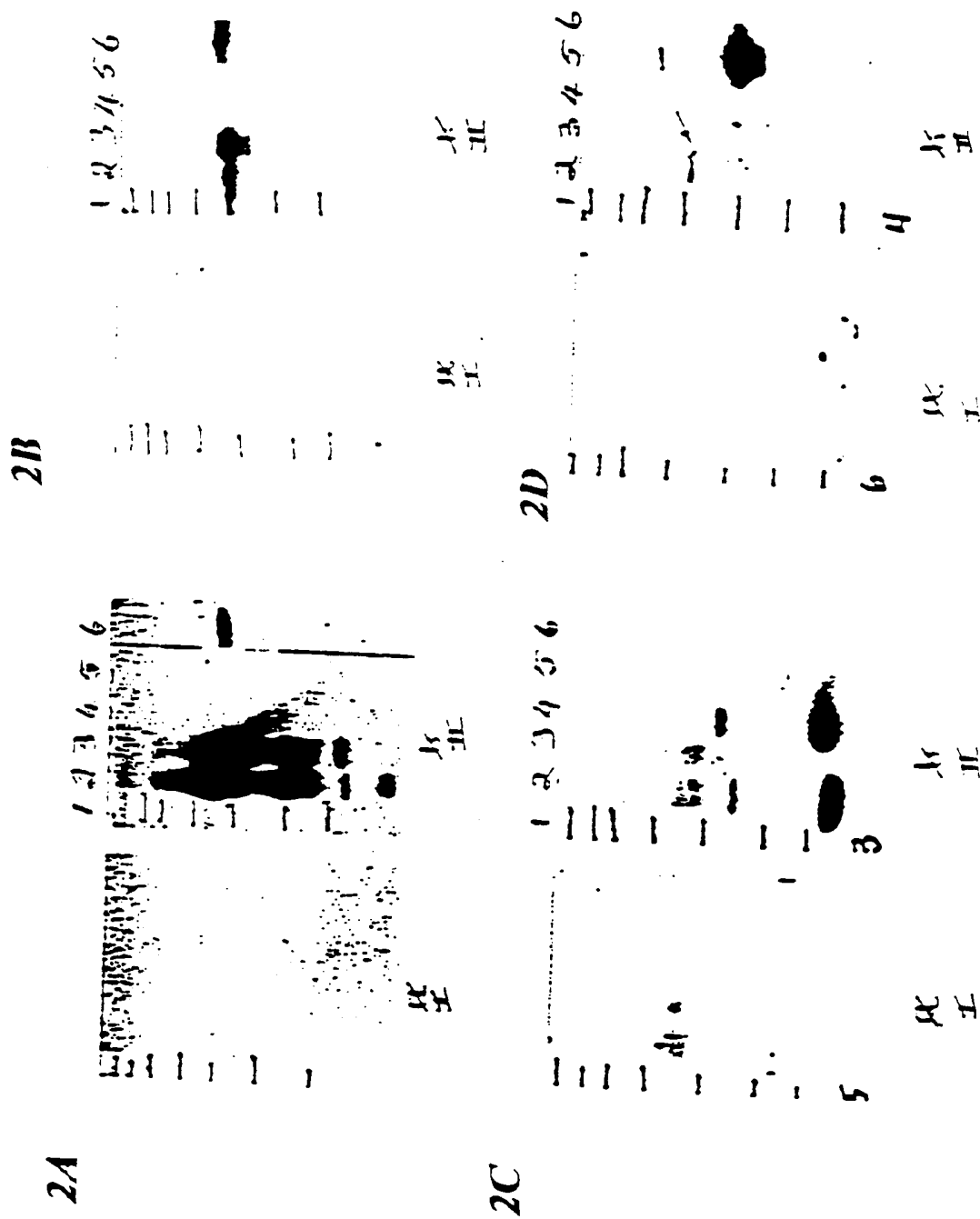


FIG. 1B



FIGS. 2A-D

T cell clone 131TbH9 responds poorly to CSP

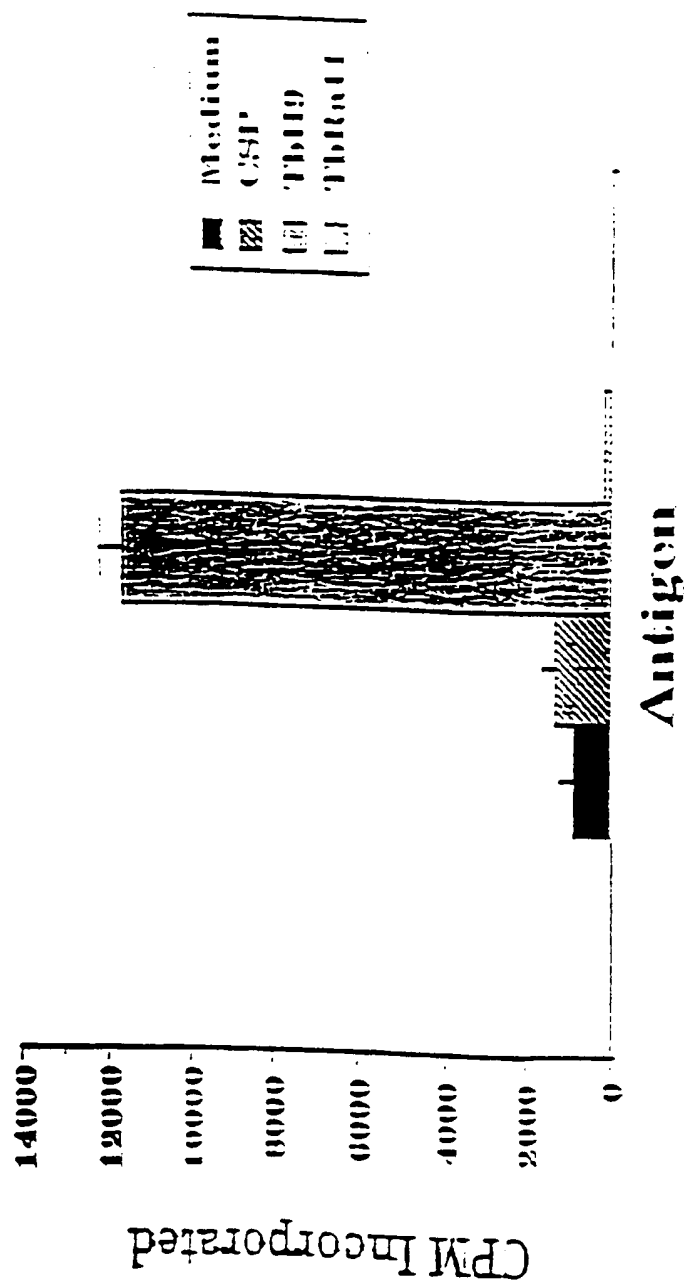


FIG. 3A

T Cell Clone PPD 800-10 IFN γ Production

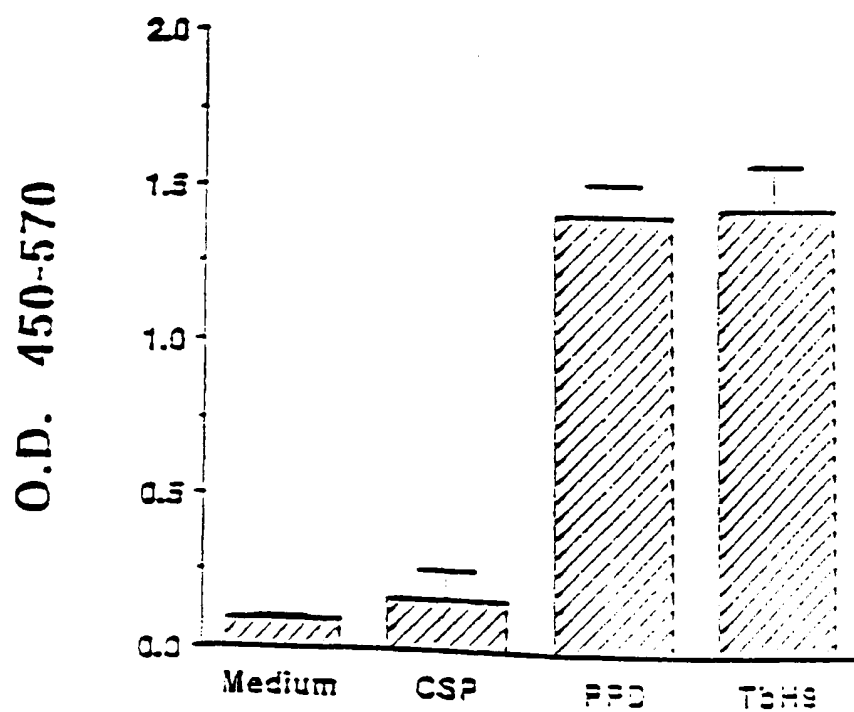


FIG. 3B

Antibody-Antigen Complexed Protein Boron

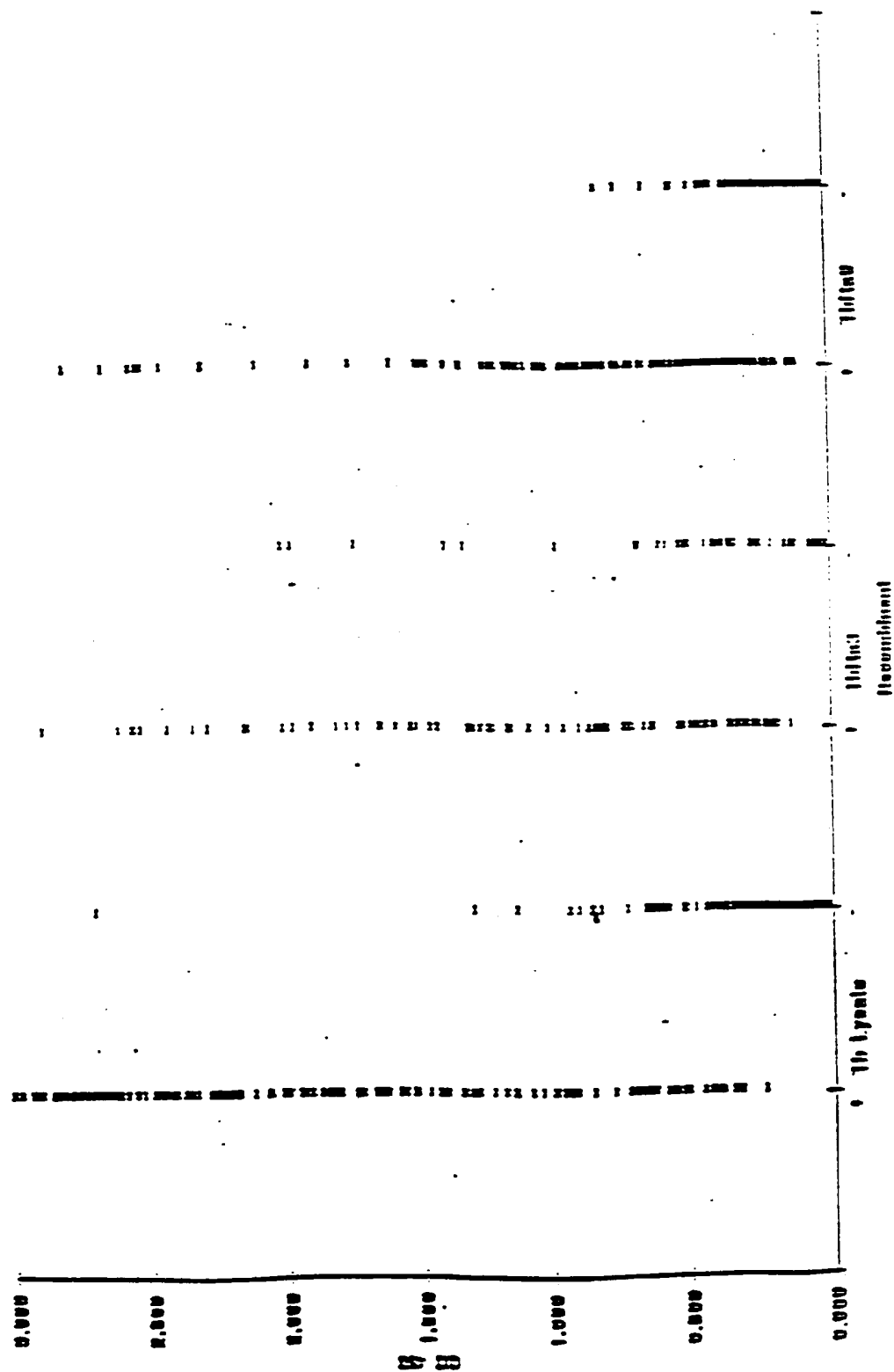


FIG. 4

FIG. 3

ELISA Sensitivity of Hexamethine and Peptide obtained using Hexamethine as a standard

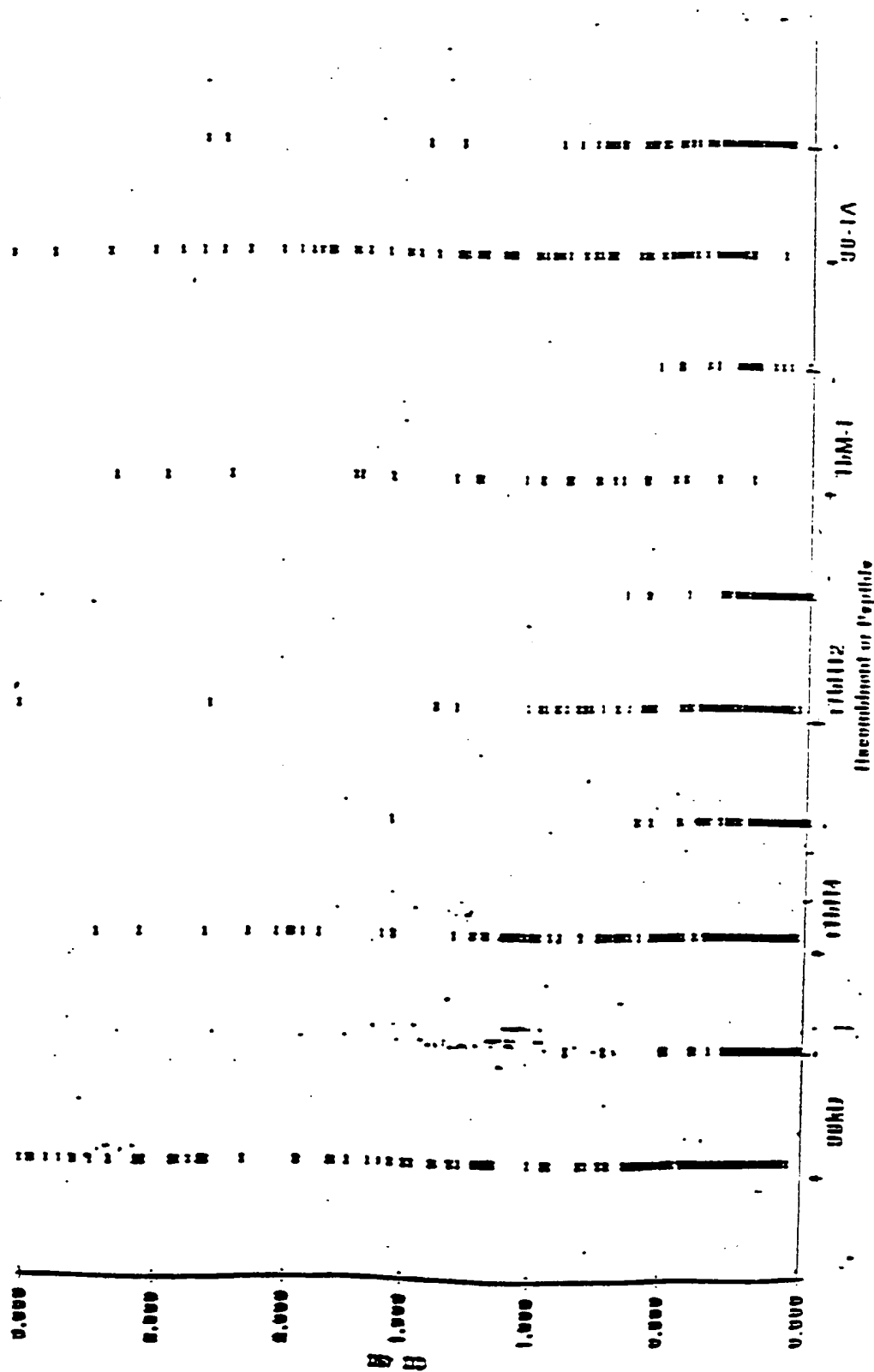


FIG. 6

Reactivity of Recombinant 30kD and TUB1a1 antigens with sera from *M. tuberculosis* patients, PPD positive and normal donors

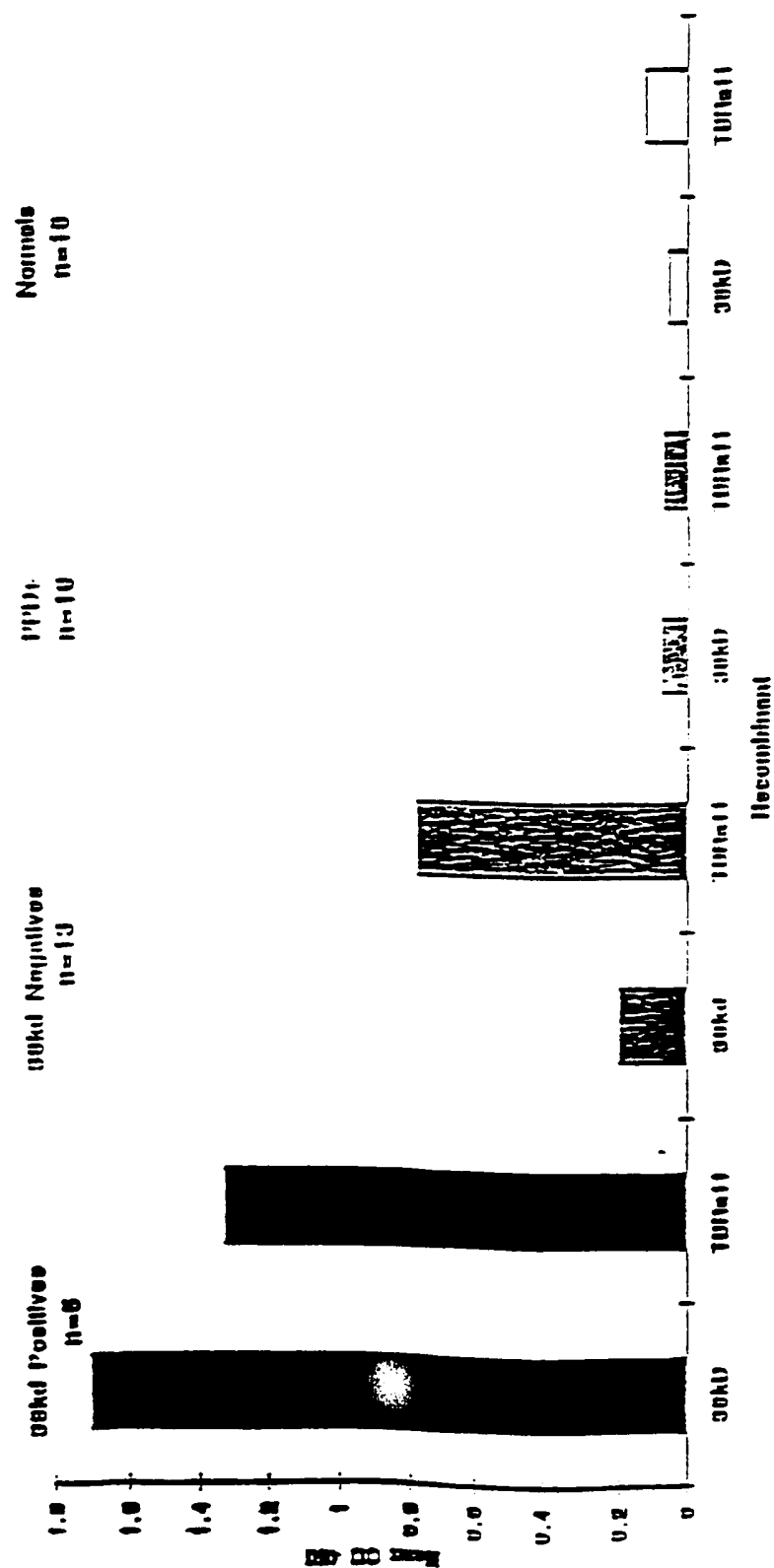
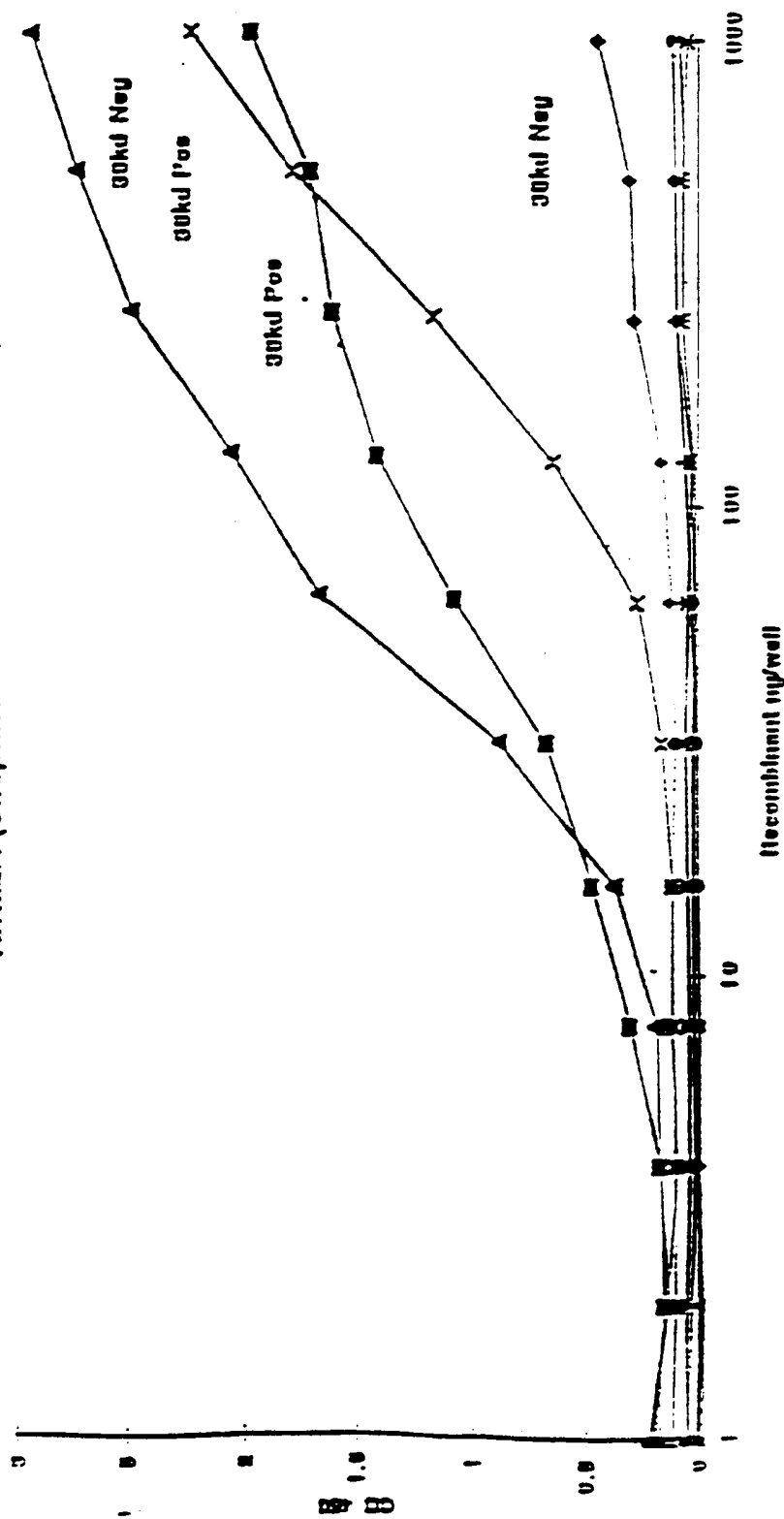


FIG. 7

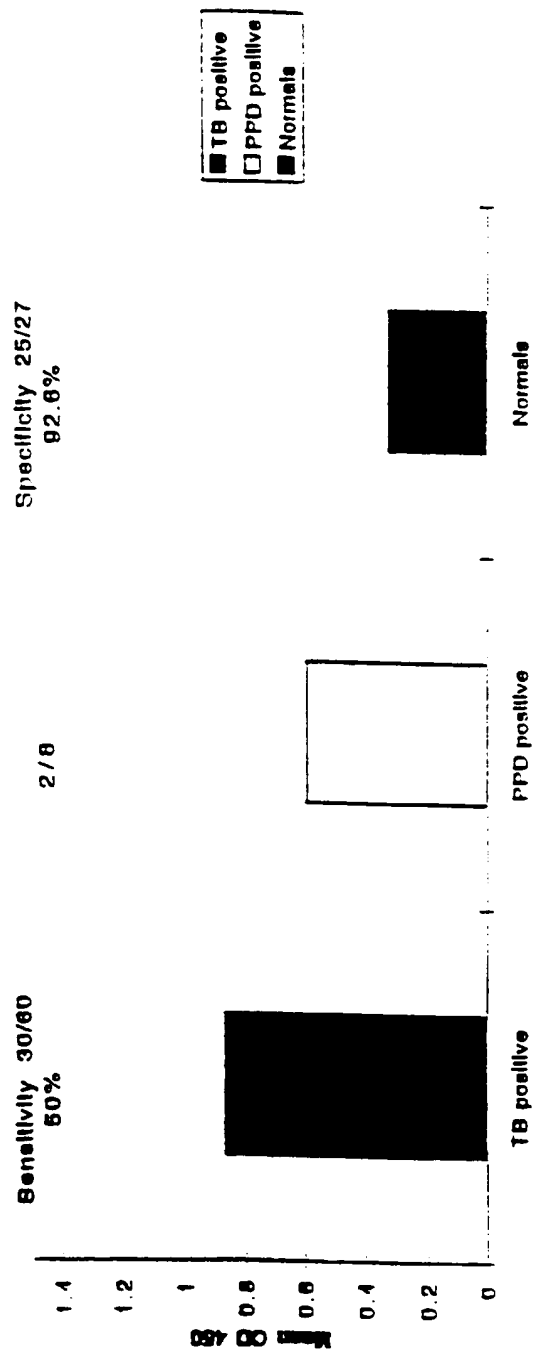
7B11a2A (Streptavidin Biotin/Protein A Biotin)



◆	10004
■	67004
▲	80004
×	30004
*	A114
●	A110
└	A140
—	A141

FIG. 9

TbH29 ELISA reactivity in Streptavidin-IMP/Protein A-biotin system



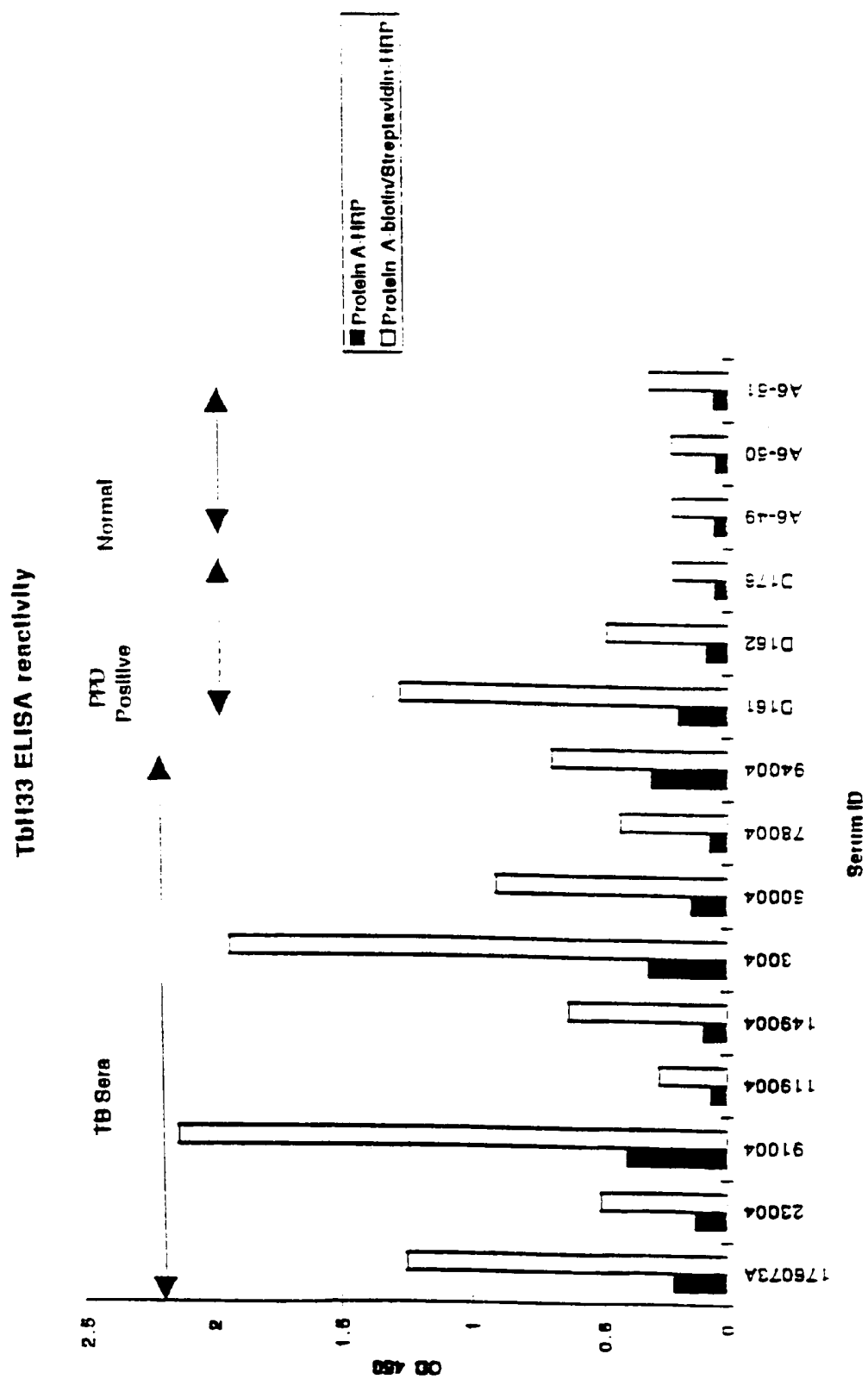
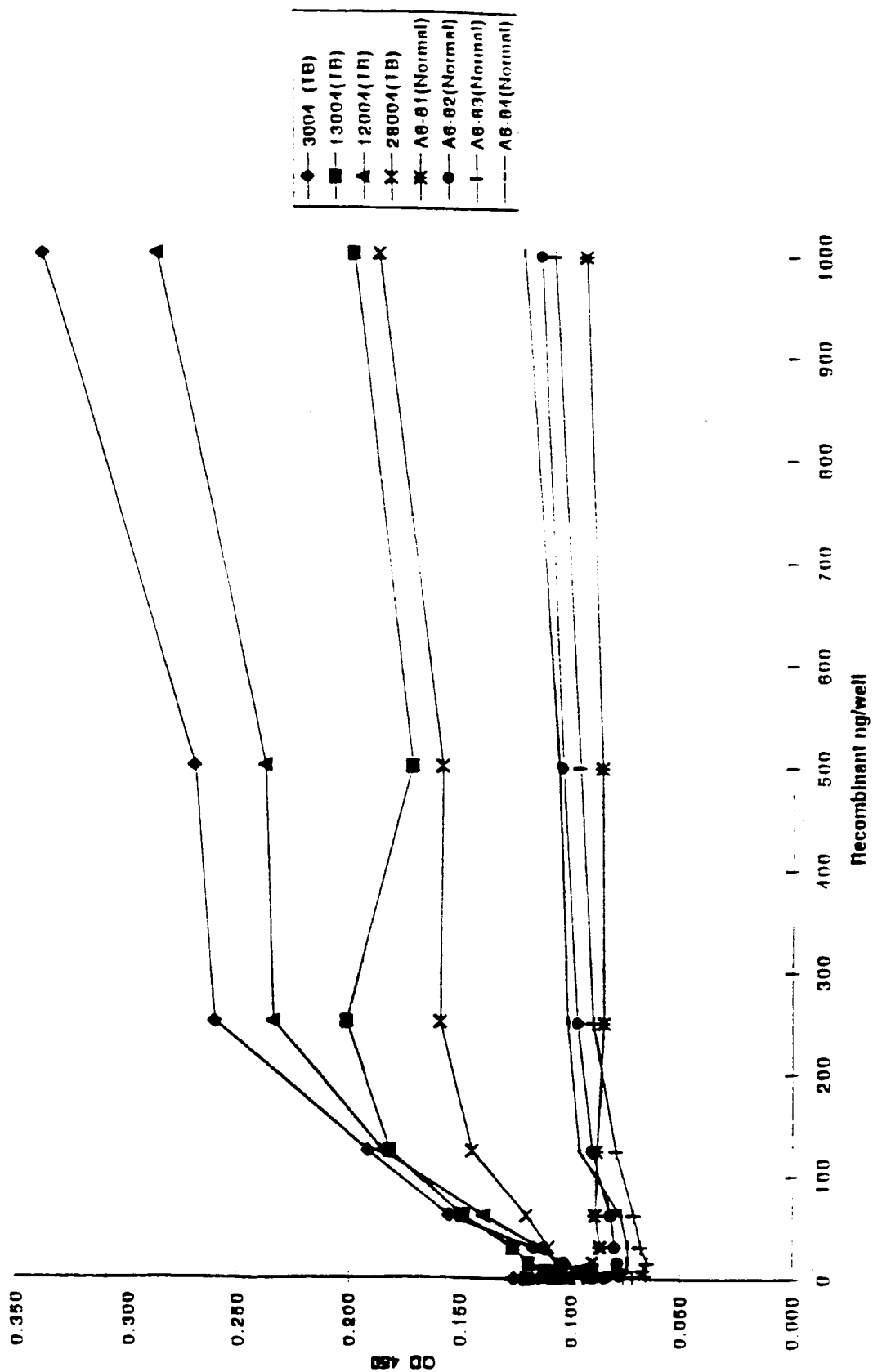


FIG. 10

ELISA reactivity of Tblt33



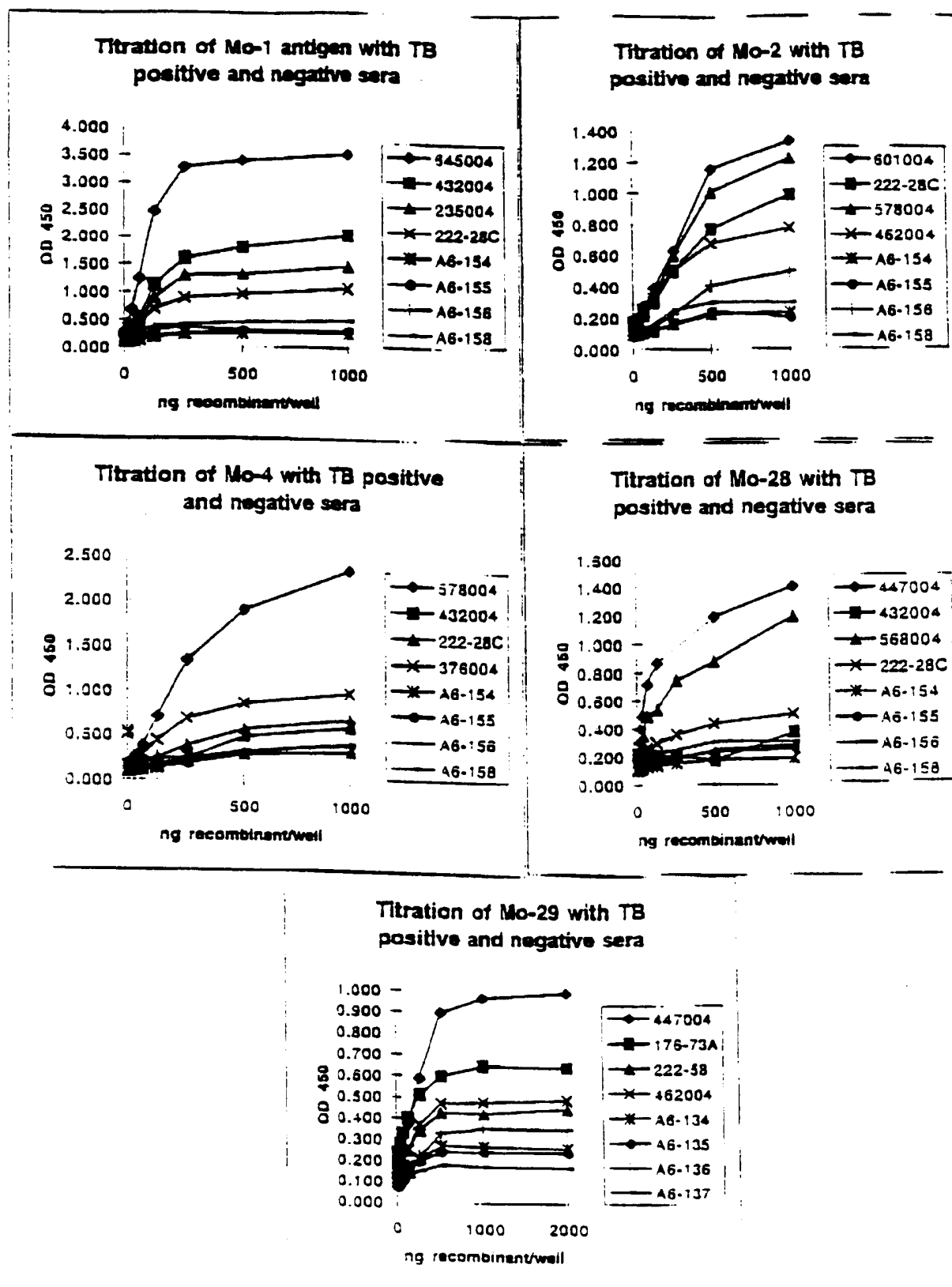


FIG 12A-12E

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald

(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 350

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 05-MAY-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.417C9

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA	60
ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC	120
GCTGCGGCCG GTGTGACTTC GATCATGGCT GCGGGCCCCG TCGTATACCA GATGCAGCCG	180
GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC	240
CCCCAGTTGA CCAGCTTGCT CAACAGCCTC GCCGATCCCA ACGTGTCTGT TCGGAACAAG	300
GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG	360
AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTCTTCA GCGTGACGAA CATCCAGCCG	420
GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCCGTCTCGG GTCCGAAGCT CTCGTGCGCC	480
GTCACGCAGA ACGTCACGTT CGTGAATCAA GCGGGCTGGA TGCTGTCACG CGCATCGGCG	540
ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CCGNTTCAGC CCGCTGTTCA	600
GCTACGCCGC CCGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG	660
GTNTGCGCAG GGNCGCACGC ACCGCCCGGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC	720
GNCACCAGNG ANCACCCCN NNTCGNCNNT TCTCGNTGNT GNATGA	766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGACCTCCGT CTTCCGCGCA	60
GACTTCCTCA GCGAGCTGGA CGCTCCTGCG CAAGCGGGTA CGGAGAGCGC GGTCTCCGGG	120
GTGGAAGGGC TCCCGCCGGG CTCGGCGTTG CTGGTAGTCA AACGAGGCC CAACGCCGGG	180
TCCCGGTTCC TACTCGACCA AGCCATCAG TCGGCTGGTC GGCATCCCGA CAGCGACATA	240
TTTCTCGACG ACGTGACCGT GAGCCGTCGC CATGCTGAAT TCCGGTTGGA AAACAACGAA	300
TTCAATGTCT TCGATGTCGG GAGTCTCAAC GGCACCTACG TCAACCGCGA GCCCGTGGAT	360
TCGGCGGTGC TGGCGAACGG CGACGAGGTC CAGATCGGCA AGCTCCGGTT GGTGTTCTTG	420
ACCGGACCCA AGCAAGGCGA GGATGACGGG AGTACCGGGG GCCCGTGAGC GCACCCGATA	480

GCCCCGCGCT GGCCGGGATG TCGATCGGGG CGGTCCCTCCG ACCTGCTACG ACCGGATT	540
TTT CCCTGATGTC CACCATCTCC AAGATTCGAT TCTTGGGAGG CTTGAGGGTC NGGGTGACCC	600
CCCCGCGGGC CTCATTCTGG GGTNTCGGCN GGTTCACCC CNTACCNACT GCCNCCCGGN	660
TTGCNAATTC NTTCTTCTNCT GCCCNNAAG GGACCNTTAN CTTGCCGCTN GAAANGGTNA	720
TCCNGGGCCC NTCCTNGAAN CCCCNTCCCC CT	752

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC ACCATCACCA TCACACTTCT AACC GCCCAG CGCGTCGGGG GCGTCGAGCA	60
CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG	120
CAGCGCGATG CCTATGTTT GTCGTCGACT CAGATATCGC GGCAATCCAA TCTCCCGCCT	180
GCGGCCGGCG GTGCTGCAAA CTA CTCCCGG AGGAATTTG ACGTGCGCAT CAAGATCTTC	240
ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGCGCCCAAG	300
ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC	360
GACCCGSCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCCGACCA GAAGTCGCTG	420
GAAAATTACA TCGCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA	480
CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG	540
CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG	600
ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG	660
CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT	720
GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCN AATGCCGGCT TGGAACCCNG	780
TGAAATTATC ACAACTTCGC AGTCACNAAA NAA	813

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC ACGGCCCGCT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCG	60
CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC	120
CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTGACA ACAACGGCAA	180
CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC	240
CGGCGACGTG ATCACC GCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA	300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG	360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG	420
ATACCACCCG CCGGCCGGCC AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC GGTGCGCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT	60
CCGGTGATCC GACSTCGCAG GTTGTGGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT	120
AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC	180
CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGGAGGT GGNCAGTCAT GCCCAGNGTG	240
ATCCAATCAA CCTGNATTCC GNCTGNGGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300
TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG	360
NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG	420
NNANNCNAN GNGTCCNAN CCCNNNTCC TCGNCGANAT CANANAGNCG NTTGATGNGA	480
NAAAAGGGTG GANCAGNNNN AANTNGNGGN CCNAANAANC NNNANNGNNG NNAGNTNGNT	540
NNNTNTTNNC ANNNNNNTG NNGNNGNCCN NNNCAANCNN NTNNNNGNAA NNGGNTTNTT	600
NAAT	604

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC	60
CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC	120
TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA	180
CGGGTGCGAA CCCTCACCT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGCGGCGCTA	240
CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC	300
ATCCTCACCG GYGCCGATCC GGTGTTCTGC GCCGGACTGG ACCTCAAGGT AGCTGGCCGG	360
GCAGACCGCG CTGCCGGACA TCTACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG	420
CGCGATCAAC GCGCGCCGG TCACCGCGG GTCGAACTG GCGCTGTACT GCGACATCCT	480
GATCGCCTCC GAGCACGCCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCCAC	540
CTGGGGACTC AGTGTGTGCT TGCCGCAAAA GGTCCGCATC GGNCTGGGCC GGTGGATGAG	600
CCTGACCGGC GACTACCTGT CCGTGACCGA CGC	633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC GCGCCGGAG AGCGGGCGCG AACGGCGATC GACGCGGCC TGGCCAGAGT	60
CGGCACCACC CAGGAGGGAG TCGAATCATG AAATTTGTCA ACCATATTGA GCCCCTCGCG	120
CCCCGCCGAG CCGGCGGCGC GGTCCCGAG GTCTATGCCG AGGCCCGCCG CGAGTTCGGC	180
CGGCTGCCCC AGCCGCTCGC CATGCTGTCC CCGGACGAGG GACTGCTCAC CGCCGGCTGG	240
GCGACGTTGC GCGAGACACT GCTGGTGGGC CAGGTGCCGC GTGGCCGCAA GGAAGCCGTC	300
GCCGCCGCCG TCGCGGCCAG CCTGCGCTGC CCCTGGTGCG TCGACGCACA CACCACCATG	360
CTGTACCGCG CAGGCCAAAC CGACACCGCC GCGGCGATCT TGGCCGGCAC AGCACCTGCC	420
GCCGGTGACC CGAACGCGCC GTATGTGGCG TGGGCGGCAG GAACCGGGAC ACCGGCGGGA	480

CCGCCGGCAC CGTTCGGCCC GGATGTCGCC GCCGAATACC TGGGCACCGC GGTGCAATTC	540
CACTTCATCG CACGCCTGGT CCTGGTGCTG CTGGACGAAA CCTTCCTGCC GGGGGGCCCCG	600
CGCGCCCAAC AGCTCATGCG CCGCGCCGGT GGAAGTGGTGT TCGCCCGCAA GGTGCGCGCG	660
GAGCATCGGC CGGGCCGCTC CACCCGCCCG CTCGAGCCGC GAACGCTGCC CGACGATCTG	720
GCATGGGCAA CACCGTCCGA GCCCATAGCA ACCGCGTTCG CCGCGCTCAG CCACCACCTG	780
GACACCGCGC CGCACCTGCC GCCACCGACT CGTCAGGTGG TCAGGCGGGT CGTGGGGTCG	840
TGGCACGGCG AGCCAATGCC GATGAGCAGT CGCTGGACGA ACGAGCACAC CGCCGAGCTG	900
CCCGCCGACC TGCACGCGCC CACCCGTCTT GCCCTGCTGA CCGGCCTGGC CCCGCATCAG	960
GTGACCGACG ACGACGTGCG CGCGGGCCGA TCCCTGCTCG ACACCGATGC GGCCTGGTT	1020
GGCGCCCTGG CCTGGGCGCG CTCACCGCC GCGCGGCGCA TCGGCACCTG GATCGGCGCC	1080
GCCGCGGAGG GCCAGGTGTC GCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCCCTGTCGG	1140
TAGGGTGTC TCGTGGCCCC GAGGGATCTC GCGGCGGCGA ACGGAGGTGG CGACACAGGT	1200
GGAAGCTGCG CCCACTGGCT TCGCCCCCAA CGCGTCTGTG GCGCTTCGGT TGGCCGCACT	1260
GGCCGATCAG GTCGGCGCCG GCCCTTGGCC GAAGGTCCAG CTCAACGTGC CGTCACCGAA	1320
GGACCGGACG GTCACCGGGG GTCACCCTGC GCGCCCAAGG AA	1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGACGCA CTCGGGCGCG	60
GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC	120
TGGATGACGT GGGCCGTGTT TACATCATCT ACCGGCAGCG GCGCGCCGAG CTGCGGACGG	180
CTAAGGCCTT GCTCGGCGTG CGGGACGAGT TAAAGCTGAG CTTGGCGGCC GTGACGGTAC	240
TGCGCGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGCCGAGTCG ACCGGCGAGC	300
TGATGGACCG ATCGGCGCGC TGTGTGCGCG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT	360
CGAGGCGGTG GGCCGAGCGG TTCGCCACGC TATTACGCAA CCTGGAATTC CTGCCGAATT	420
CGCCACGTT GATGAATCT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTTGTTCTGC	480

CGATTGAGGA TTCGCTGCAA TCGATCTTTG CGACGCTGGG ACAGGCCGCC GAGCTGCAGC	540
GGGCTGGAGG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG	600
CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTCGTTTCT ACGGCTGTAT GACAGTGCCG	660
CGGGTGTGGT CTCCATGGGC GGTGCGCGGC GTGGCGCCTG TATGGCTGTG CTTGATGTGT	720
CGCACCCGGA TATCTGTGAT TTCGTCACCG CCAAGGCCGA ATCCCCCAGC GAGCTCCCCG	780
ATTTCAACCT ATCGGTTGGT GTGACCGACG CGTTCCTGCG GGCCGTCGAA CGCAACGGCC	840
TACACCGGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC GCGGATGCCC GCCGCCGAGC	900
TGTTGACGCG CATCTGCAA GCGCGCACG CCGGTGGCGA TCCCGGGCTG GTGTTTCTCG	960
ACACGATCAA TAGGGCAAAC CCGGTGCCCG GGAGAGGCCG CATCGAGGCG ACCAACCCST	1020
GCGGGGAGGT CCCACTGCTG CTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC	1080
GGATGCTCGC CGACGGTCGC GTCGACTGGG ACCGGCTCGA GGAGGTCGCC GGTGTGGCGG	1140
TGCGGTTTCT TGATGACGTC ATCGATGTCA GCCGCTACCC CTTCCCCGAA CTGGGTGAGG	1200
CGGCCCGCGC CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG	1260
CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATGCGTC	1320
GCATACAGCA GCGGCGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GCGCATTTCC	1380
CGCGGTTTAC CGATAGCCGG TTCGCGCGGT CGGGCCCGAG GCGCAACGCA CAGGTCACCT	1440
CCGTCGCTCC GACGGGCA	1458

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAT CGTGCTGGAT CTGGAACCGC GTGGCCCCGT ACCTACCGAG ATCTACTGGC	60
GCGCAGGGG GCTGGCCCTG GGCATCGCGG TCGTCGTAGT CGGGATCGCG GTGGCCATCG	120
TCATCGCCTT CGTCGACAGC AGCGCCGGTG CCAAACCGGT CAGCGCCGAC AAGCCGGCCT	180
CCGCCCAGAG CCATCCGGGC TCGCCGGCAC CCCAAGCACC CCAGCCGGCC GGGCAAACCG	240
AAGGTAACGC CGCCGCGGCC CCGCCGAGG GCCAAAACCC CGAGACACCC ACGCCACCG	300

CCGCGGTGCA GCCGCCGCCG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG	360
CCGTCAAAGG TTTGACCAAC GCGCCGCAGT ACTACGTCGG CGACCAGCCG AAGTTCACCA	420
TGGTGGTCAC CAACATCGGC CTGGTGTCTT GTAAACGCGA CGTTGGGGCC GCGGTGTTGG	480
CCGCCTACGT TTA CTGCTG GACAACAAGC GGTGTGTGGT CAACCTGGAC TGCGCGCCCT	540
CGAATGAGAC GCTGGTCAAG ACGTTTTCCT CCGGTGAGCA GGTAACGACC GCGGTGACCT	600
GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA	660
CCTACAATCT CGTGGTACAA CTGGGCAATC TGCGCTCGCT GCCGGTTCCG TTCATCCTGA	720
ATCAGCCGCC GCCGCCGCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC	780
CGGAGTCTCC CCGCAAGGC GGATAATTAT TGATCGCTGA TGGTCGATTC CGCCAGCTGT	840
GACAACCCCT CGCCTCGTGC CG	862

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC CAATGACAAA	60
GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC GAACGCTGGA	120
GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG CGCGGACGCG	180
TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GGCGCCACGG TGGCGCTAAC CTTTCAGGAT	240
CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA GTGATGAAGG	300
TGCGCCGCGCA GTGTTCAAAG CTCGGATATA CCGTGGCACC CATGGAACAG CGTGCGGAGT	360
TGGTGGTTGG CCGGGCACTT GTCGTCGTCG TTGACGATCG CACGGCGCAC GGCGATGAAG	420
ACCACAGCGG GCCGCTTGTC ACCGAGCTGC TCACCGAGGC CGGGTTTGTT GTCGACGGCG	480
TGGTGGCGGT GTCGGCCGAC GAGGTCGAGA TCCGAAATGC GCTGAACACA GCGGTGATCG	540
GCGGGGTGGA CCTGGTGGTG TCGGTCGGCG GGACCGGNGT GACGNCTCGC GATGTCACCC	600
CGGAAGCCAC CCGNGACATT CT	622

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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GGCGCAGCGG TAAGCCTGTT GGCCGCCGGC AACTGGTGT TGACAGCATG CGGCGGTGGC      60
ACCAACAGCT CGTCGTCAGG CGCAGGCGGA ACGTCTGGGT CGGTGCACTG CGGCGGCAAG      120
AAGGAGCTCC ACTCCAGCGG CTCGACCGCA CAAGAAAATG CCATGGAGCA GTTCGTCTAT      180
GCCTACGTGC GATCGTGCCC GGGCTACACG TTGGACTACA ACGCCAACGG GTCCGGTGCC      240
GGGGTGACCC AGTTTCTCAA CAACGAAACC GATTTCGCCG GCTCGGATGT CCCGTTGAAT      300
CCGTCGACCG GTCAACCTGA CCGGTCGGCG GAGCGGTGCG GTTCCCCGGC ATGGGACCTG      360
CCGACGGTGT TCGGCCCCGAT CGCGATCACC TACAATATCA AGGGCGTGAG CACGCTGAAT      420
CTTGACGGAC CCACTACCGC CAAGATTTTC AACGGCACCA TCACCGTGTG GAATGATCCA      480
CAGATCCAAG CCCTCAACTC CGGCACCGAC CTGCCGCCAA CACCGATTAG CGTTATCTTC      540
CGCAGCGACA AGTCCGGTAC GTCGGACAAC TTCCAGAAAT ACCTCGACGG TGTATCCAAC      600
GGGGCGTGGG GCAAAGGCGC CAGCGAAACG TTCAGCGGGG GCGTCGGCGT CGGCGCCAGC      660
GGGAACAACG GAACGTCGGC CCTACTGCAG ACGACCGACG GGTCGATCAC CTACAACGAG      720
TGGTCGTTTG CGGTGGGTAA GCAGTTGAAC ATGGCCCAGA TCATCACGTC GGCGGGTCCG      780
GATCCAGTGG CGATCACCAC CGAGTCGGTC GGTAAGACAA TCGCCGGGGC CAAGATCATG      840
GGACAAGGCA ACGACCTGGT ATTGGACACG TCGTCTGTCT ACAGACCCAC CCAGCCTGGC      900
TCTTACCCGA TCGTGCTGGC GACCTATGAG ATCGTCTGCT CGAAATACCC GGATGCGACG      960
ACCGGTACTG CGGTAAGGGC GTTTATGCAA GCCGCGATTG GTCCAGGCCA AGAAGGCCTG     1020
GACCAATACG GCTCCATTCC GTTGCCCCAA TCGTTCCAAG CAAAATTGGC GGCCGCGGTG     1080
AATGCTATTT CTTGACCTAG TGAAGGGAAT TCGACGGTGA GCGATGCCGT TCCGCAGGTA     1140
GGGTCGCAAT TTGGGCCGTA TCAGCTATTG CGGCTGCTGG GCCGAGGCGG GATGGGCGAG     1200

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT GCAGGTCGTG CTGTTGACG AACTGGGCAT GCCGAAGACC AAACGCACCA	60
AGACCGGCTA CACCACGGAT GCCGACGCGC TGCAGTCGTT GTTCGACAAG ACCGGGCATC	120
CGTTTCTGCA ACATCTGCTC GCCCACC GCG ACGTCACCCG GCTCAAGGTC ACCGTCGACG	180
GGTTGCTCCA AGCGGTGGCC GCCGACGGCC GCATCCACAC CACGTTCAAC CAGACGATCG	240
CCGCGACCGG CCGGCTCTCC TCGACCGAAC CCAACCTGCA GAACATCCCG ATCCGCACCG	300
ACGCGGGCCG GCGGATCCG GACGCGTTCG TGGTCGGGGA CGGTTACGCC GAGTTGATGA	360
CGGCCGACTA CAGCCAGATC GAGATGCGGA TCATGGGGCA CCTGTCCGGG GACGAGGGCC	420
TCATCGAGGC GTTCAACACC GGGGAGGACC TGTATTCGTT CGTCGCGTCC CGGGTGTTCG	480
TGTGCCCCAT CGACGAGGTC ACCGGCGAGT TCGCGC3CCG GGTCAAGGCG ATGTCCTACG	540
GGCTGGTTTA CGGGTTGAGC GCCTACGGCC TGTCGCAGCA GTTGAAAATC TCCACCGAGG	600
AAGCCAACGA GCAGATGGAC GCGTATTTTCG CCCGATTCCG CGGGGTGCGC GACTACCTGC	660
GCGCCGTAGT CGAGCGGGCC CGCAAGGACG GCTACACCTC GACGGTGCTG GGCCGTCGCC	720
GCTACCTGCC CGAGCTGGAC AGCAGCAACC GTCAAGTGCG GGAGGCCGCC GAGCGGGCGG	780
CGCTGAACGC GCCGATCCAG GGCAGCGCGG CCGACATCAT CAAGGTGGCC ATGATCCAGG	840
TCGACAAGGC GCTCAACGAG GCACAGCTGG CGTCGCGCAT GCTGCTGCAG GTCCACGACG	900
AGCTGCTGTT CGAAATCGCC CCCGGTGAAC GCGAGCGGGT CGAGGCCCTG GTGCGCGACA	960
AGATGGGCGG CGGTTACCCG CTCGACGTCC CGCTGGAGGT GTCGGTGGGC TACGGCCGCA	1020
GCTGGGACGC GGCGGCGCAC TGAGTGCCGA GCGTGATCT GGGGCGGGAA TTCGGCGATT	1080
TTTCCGCCCT GAGTTCACGC TCGGCGCAAT CGGGACCGAG TTTGTCCAGC GTGTACCCGT	1140
CGAGTAGCCT CGTCA	1155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC TGGTGTTTGA ACGGTTTTAC CGGTCGGCAT CGGCACGGGC GTTGCCGGGT	60
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TCGGGCCTCG GGTGGCGAT CGTCAAACAG GTGGTGCTCA ACCACGGCGG ATTGCTGCGC	120
ATCGAAGACA CCGACCCAGG CGGCCAGCCC CCTGGAACGT CGATTACGT GCTGCTCCCC	180
GGCCGTCGGA TGCCGATTCC GCAGCTTCCC GGTGCGACGG CTGGCGCTCG GAGCACGGAC	240
ATCGAGAACT CTCGGGGTTC GGCGAACGTT ATCTCAGTGG AATCTCAGTC CACGCGCGCA	300
ACCTAGTTGT GCAGTTACTG TTGAAAGCCA CACCCATGCC AGTCCACGCA TGGCCAAGTT	360
GGCCCCAGTA GTGGGCCTAG TACAGGAAGA GCAACCTAGC GACATGACGA ATCACCCACG	420
GTATTCGCCA CCGCCGACG AGCCGGGAAC CCCAGGTTAT GCTCAGGGGC AGCAGCAAAC	480
GTACAGCCAG CAGTTCGACT GGC GTTACCC ACCGTCCCCG CCCCCGACG CAACCCAGTA	540
CCGTCAACCC TACGAGGCGT TGGGTGGTAC CCGGCCGGGT CTGATACCTG GCGTGATTCC	600
GACCATGACG CCCCCTCCTG GGATGGTTCG CCAACGCCCT CGTGCAGGCA TGTGGCCAT	660
CGGCGCGGTG ACGATAGCGG TGGTGTCCGC CGGCATCGGC GCGCGGGCCG CATCCCTGGT	720
CGGGTTCAAC CGGGCACCCG CCGGCCCCAG CGGCGGCCCA GTGGCTGCCA GCGCGGCGCC	780
AAGCATCCCC GCAGCAAACA TGCCGCCGGG GTCGGTCGAA CAGGTGGCGG CCAAGGTGGT	840
GCCCAGTGTC GTCATGTTGG AAACCGATCT GGGCCGCCAG TCGGAGGAGG GCTCCGGCAT	900
CATTCTGTCT GCCGAGGGGC TGATCTTGAC CAACAACCAC GTGATCGCGG CGGCCGCCAA	960
GCCTCCCTG GGCAGTCCGC CGCCGAAAAC GACGGTAACC TTCTCTGACG GCGGACCCG	1020
ACCCTTCACG GTGGTGGGG CTGACCCAC CAGTGATATC GCCGTCTGCC GTGTTACAGG	1080
CGTCTCCGGG CTCACCCCGA TCTCCCTGGG TTCCTCCTCG GACCTGAGGG TCGGTCAGCC	1140
GGTGCTGGCG ATCGGGTCGC CGCTCGGTTT GGAGGGCACC GTGACCACGG GGATCGTCAG	1200
CGCTCTCAAC CGTCCAGTGT CGACGACCGG CGAGGCCGGC AACCAGAACA CCGTGCTGGA	1260
CGCCATTGAG ACCGACGCCG CGATCAACCC CGGTAACCTC GGGGGCGCGC TGGTGAACAT	1320
GAACGCTCAA CTCGTGCGAG TCAACTCGGC CATTGCCACG CTGGGCGCGG ACTCAGCCGA	1380
TGCGCAGAGC GGCTCGATCG GTCTCGGTTT TGGGATTCCA GTCGACCAGG CCAAGCGCAT	1440
CGCCGACGAG TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC	1500
CAATGACAAA GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC	1560
GAACGCTGGA GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG	1620
CGCGGACGCG TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GCGGCCACGG TGGCGCTAAC	1680
CTTTCAGGAT CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA	1740

GTGATGAAGG TCGCCGCGCA GTGTTCAAAG C

1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG GTGGCGGCGG CTCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTCGGC	60
ACGAGGATCC GACGTCGAG GTTGTGCAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT	120
AGCCCCGGCG CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GCGGGCAAT TTGGCGGGGC	180
CCGGCGACGG CGAGCGCCGG AATGGCGCGA GTGAGGAGGC GGGCAGTCAT GCCCAGCGTG	240
ATCCAATCAA CCTGCATTCG GCCTGCGGGC CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300
TGAATGATGG AAAACGGGCG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCCTGG	360
CGTTGTGGCT ATCAGGATGT TCTTCGCCGA AACCTGATGC CGAGGAACAG GGTGTTCCCCG	420
TGAGCCCGAC GCGTCCGAC CCCGCGCTCC TCGCCGAGAT CAGGCAGTCG CTTGATGCCA	480
CAAAAGGGTT GACCAGCGTG CACGTAGCGG TCCGAACAAC CGGGAAAGTC GACAGCTTGC	540
TGGGTATTAC CAGTSCCAT STCGACGTCC GGGCCAATCC GCTCGCGCA AAGGGCGTAT	600
GCACCTACAA CGACGAGCAG GGTGTCCCGT TTCGGGTACA AGGCGACAAC ATCTCGGTGA	660
AACTGTTCCA CGACTGGAGC AATCTCGGCT CGATTTCTGA ACTGTCAACT TCACGCGTGC	720
TCGATCCTGC CGCTGGGGTG ACGCAGCTGC TGTCCGGTGT CACGAACCTC CAAGCGCAAG	780
GTACCGAAGT GATAGACGGA ATTTGACCA CCAAATCAC CGGGACCATC CCCGCGAGCT	840
CTGTCAAGAT GCTTGATCCT GCGCCCAAGA GTGCAAGGCC GCGGACCGTG TGGATTGCCC	900
AGGACGGCTC GCACCACCTC GTCCGAGCGA GCATCGACCT CGGATCCGGG TCGATTGAGC	960
TCACGCAGTC GAAATGGAAC GAACCCGTCA ACGTCGACTA GGCCGAAGTT GCGTCGACGC	1020
GTTGNTCGAA ACGCCCTTGT GAACGGTGTC AACGGNAC	1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGGAACAGGC	60
GGCGGCGGAG GCGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT	120
CATTGAGCAG GACATGGCCG TGGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA	180
AGTGTCTGTT AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCCGGCGA GCAAGACGCA	240
AAATCGCACG GTTTGCGGTT GATTCGTGCG ATTTTGTGTC TGCTCGCCGA GGCCTACCAG	300
GCGCGGCCCA GGTCCGCGTG CTGCCGTATC CAGGCGTGCA TCGCGATTCC GCGCGCCACG	360
CCGGAGTTAA TGCTTCGCGT CGACCCGAAC TGGGCGATCC GCCGGNGAGC TGATCGATGA	420
CCGTGGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGGTAGGA	480
AGCGTCCGTA GGCGGCGGTG CTGACCGGCT CTGCCTGCGC CCTCAGTGC GGCAGCGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCCGCC CGCGCCTCCG TTGCCCCCAT TGCCGCCGTC GCCGATCAGC TGCGCATCGC	60
CACCATCACC GCCTTTGCCG CCGGCACCGC CGGTGGCGCC GGGGCCGCCG ATGCCACCGC	120
TTGACCCTGG CCGCCGGCGC CGCCATTGCC ATACAGCACC CCGCCGGGGG CACCGTTACC	180
GCCGTCGCCA CCGTCGCCGC CGCTGCCGTT TCAGGCCGGG GAGGCCGAAT GAACCGCCGC	240
CAAGCCCGCC GCCGGCACCG TTGCCGCCTT TTCCGCCCGC CCCGCCGGCG CCGCCAATTG	300
CCGAACAGCC AMGCACCGTT GCCGCCAGCC CCGCCGCCGT TAACGGCGCT GCCGGGCGCC	360
GCCGCCGGAC CCGCCATTAC CGCCGTTCCC GTTCGGTGCC CCGCCGTTAC CGGCGCCGCC	420
GTTTGCCGCC AATATTCGGC GGGCACCGCC AGACCCGCCG GGGCCACCAT TGCCGCCGGG	480
CACCGAAACA ACAGCCCAAC GGTGCCGCCG GCCCCGCCGT TTGCCGCCAT CACCGGCCAT	540
TCACCGCCAG CACCGCCGTT AATGTTTATG AACCCGGTAC CGCCAGCGCG GCCCCTATTG	600
CCGGGCGCCG GAGNGCSTGC CCGCCGGCGC CGCCAACGCC CAAAAGCCCG GGGTTGCCAC	660

CGGCCCCGCC GGACCCACCG GTCCCGCCGA TCCCCCGTT GCCGCCGGTG CCGCCGCCAT	720
TGGTGCTGCT GAAGCCGTTA GCGCCGGTTC CGCSGGTTCC GGCGGTGGCG CCNTGGCCGC	780
CGGCCCCGCC GTTGCCGTAC AGCCACCCCC CGGTGGCGCC GTTGCCGCCA TTGCCGCCAT	840
TGCCGCCGTT GCCGCCATTG CCGCCGTTCC CGCCGCCACC GCCGNTTGG CCGCCGGCGC	900
CGCCGGCGGC CGC	913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG GTGTAGAAAA ATCCTGCCGC CCGGACCCTT AAGGCTGGGA CAATTTCTGA	60
TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTCC CGCCGCCGCT CACTCAGGTG	120
GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCCA	180
GGCGGCCCCG CCGGCCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TGCCCCCTCGA	240
CCCGTCCGCG ATGGTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAAGTGGG	300
CTACAACAAC GCCGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTCGTGCT	360
GACCAACAAC CACGTGATCG CGGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG	420
CCAAACCTAC GGCCTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCG CGGTGCTGCA	480
GCTGCGCGGT GCCGGTGGCC TGCCGTCGGC GGCSATCGGT GGCGGCGTCG CGGTTGGTGA	540
GCCCCTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTC CGGTGCCTGG	600
CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GCGCTCGGAT TCGCTGACCG GTGCCGAAGA	660
GACATTGAAC GGGTTGATCC AGTTCGATGC CGCAATCCAG CCCGGTGATT CGGGCGGGCC	720
CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCCGCGTCCG ATAACCTCCA	780
GCTGTCCCAG GGTGGGCAGG GATTCGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG	840
CCAAATCCGA TCGGGTGGGG GGTCACCCAC CGTTCATATC GGGCCTACCG CCTTCCTCGG	900
CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCACGAGTC CAACGCGTGG TCGGAAGCGC	960
TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTGG ACGGCGCTCC	1020

GATCAACTCG GCCACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCAT 1080
CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGGAACTGA CATTGGCCGA 1140
GGGACCCCCG GCCTGATTTG TCGCGGATAC CACCCGCCGG CCGGCCAATT GGATTGGCGC 1200
CAGCCGTGAT TGCCGCGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA 1260
GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA 1320
GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCCGC 1380
GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC 1440
GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGAATCATCG ATCGCCTCGA CTACCTGCAG 1500
TGGCTTGGCA TCGACTGCAT CTGTTGCCGC CGTTCCTACG ACTCACCGCT GCGCGACGGC 1560
GGTTACGACA TTCGCGACTT CTACAAGGTG CTGCCCCAAT TCGGCACCGT CGACGATTTC 1620
GTGCCCCTGG TCGACACCGC TCACCGCGCA GGTATCCGCA TCATCACCGA CCTGGTGATG 1680
AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCGCGACCC AGACGGACCG 1740
TACGGTGACT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC 1800
TTCGTCGACA CCGAAGAGTC GAACTGGTCA TTCGATCCTG TCCGCCGACA GTTINCTACTG 1860
GCACCGATTG TT 1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA ACCTGATGCC GAGGAACAGG GTGTTCCCGT GAGCCCGACG GCGTCCGACC 60
CCGCGCTCCT CGCCGAGATC AGGCAGTCGC TTGATGCGAC AAAAGGGTTG ACCAGCGTGC 120
ACGTAGCGGT CCGAACAACC GGGAAAGTCG ACAGCTTGCT GGGTATTACC AGTGCCGATG 180
TCGACGTCCG GGCCAATCCG CTCGCGGCAA AGGGCGTATG CACCTACAAC GACGAGCAGG 240
GTGTCCCGTT TCGGGTACAA GGCGACAACA TCTCGGTGAA ACTGTTGAC GACTGGAGCA 300
ATCTCGGCTC GATTTCTGAA CTGTCAACTT CACGCGTGCT CGATCCTGCC GCTGGGGTGA 360
CGCAGCTGCT GTCCGGTGTC ACGAACCTCC AAGCGCAAGG TACCGAAGTG ATAGACGGAA 420
TTTCGACCAC CAAAATCACC GGGACCATCC CCGCGAGCTC TGTCAAGATG CTTGATCCTG 480

GCGCCAAGAG TGCAAGGCCG GCGACCGTGT GGATTGCCCA GGACGGCTCG CACCACCTCG	540
TCCGAGCGAG CATCGACCTC GGATCCGGGT CGATTCAGCT CACGCAGTCG AAATGGAACG	600
AACCCGTCAA CGTCGACTAG GCCGAAGTTG CGTCGACGCG TTGCTCGAAA CGCCCTTGTC	660
AACGGTGTCA ACGGCACCCG AAAACTGACC CCCTGACGGC ATCTGAAAAT TGACCCCTTA	720
GACCGGGCGG TTGGTGGTTA TTCTTCGGTG GTTCCGGCTG GTGGGACGCG GCCGAGGTCG	780
CGGTCTTTGA GCCGGTAGCT GTCGCCTTTG AGGGCGACGA CTTCAGCATG GTGGACGAGG	840
CGGTGATCA TGGCGGCAGC AACGACGTCG TCGCCGCCGA AAACCTCGCC CCACCGGCCG	900
AAGGCCTTAT TGGACGTGAC GATCAAGCTG GCCCCTCAT ACCGGGAGGA CACCAGCTGG	960
AAGAAGAGGT TGGCGGCCTC GGGCTCAAAC GGAATGTAAC CGACTTCGTC AACCACCAGG	1020
AGCGGATAGC GGCCAAACCG GGTGAGTTG GCGTAGATGC GCCCGGCGTG GTGAGCCTCG	1080
GCGAACCGTG CTACCCATTC GCGCGCGGTG GCGAACAGCA CCCGATGACC GGCCTGACAC	1140
GCGCGTATCG CCAGGCCGAC CGCAAGATGA GTCTTCCCCG TGCCAGGCGG GGCCCAAAAA	1200
CACGACGTTA TCGCGGGCGG TGATGAAATC CAGGGTGCCC AGATGTGCGA TGGTGTGCGG	1260
TTTGAGGCCA CGAGCATGCT CAAAGTCGAA CTCTTCCAAC GACTTCCGAA CCGGGAAGCG	1320
GGCGGCGCGG ATGCGGCCCT CACCACCATG GGAATCCCCG GCTGACACTT CCCGCTGCAG	1380
GCAGGCGGCC AGGTATTCTT CGTGGCTCCA GTTCTCGGCG CGGGCGCGAT CGGCCAGCCG	1440
GGAACTGAC TCACGCAGGG TGGGAGCTTT CAATGCTCTT GT	1482

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 976 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA CGAGCCGGCG ATAGCTTCTG GGCCGCGGCC GACCAGATGG CTCGAGGGTT	60
CGTGCTCGGG GCCACCGCCG GGCGCACCAC CCTGACCGGT GAGGGCCTGC AACACGCCGA	120
CGGTCACTCG TTGCTGCTGG ACGCCACCAA CCCGGCGGTG GTTGCTTACG ACCCGGCCTT	180
CGCCTACGAA ATCGGCTACA TCGNGGAAAG CGGACTGGCC AGGATGTGCG GGGAGAACCC	240
GGAGAACATC TTCTTCTACA TCACCGTCTA CAACGAGCCG TACGTGCAGC CGCCGGAGCC	300

GGAGAACTTC GATCCCGAGG GCGTGCTGGG GGGTATCTAC CGNTATCAG CGGCCACCGA 360
 GCAACGCACC AACAAGGNGC AGATCCTGGC CTCCGGGGTA GCGATGCCCC CGGCGCTGCG 420
 GGCAGCACAG ATGCTGGCCG CCGAGTGGGA TGTCGCCGCC GACGTGTGGT CGGTGACCAG 480
 TTGGGGCGAG CTAAACCGCG ACGGGGTGGT CATCGAGACC GAGAAGCTCC GCCACCCCGA 540
 TCGGCCGGCG GCGTGCCCT ACGTGACGAG AGCGCTGGAG AATGCTCGGG GCCCGGTGAT 600
 CGCGGTGTGC GACTGGATGC GCGCGTCCC CGAGCAGATC CGACCGTGGG TGCCGGGCAC 660
 ATACCTCAG TTGGGCACCG ACGGGTTCGG TTTTCCGAC ACTCGGCCCC CCGGTCTGTCG 720
 TTACTTCAAC ACCGACGCCG AATCCCAGGT TGGTCGCGGT TTTGGGAGGG GTTGGCCGGG 780
 TCGACGGGTG AATATCGACC CATTGGGTGC CGGTCTGGG CCGCCCGCCC AGTTACCCGG 840
 ATTCGACGAA GGTGGGGGGT TCGCCCCGAN TAAGTT 876

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG GCTGCAGGAA TTCGGCACGA GAGACAAAAT TCCACGCGTT AATGCAGGAA 60
 CAGATTCATA ACGAATTCAC AGCGGCACAA CAATATGTCT CGATCGCGGT TTATTTTCGAC 120
 AGCGAAGACC TGCCGCAGTT GGCGAAGCAT TTTTACAGCC AAGCGGTCTGA GGAACGAAAC 180
 CATGCAATGA TGCTCTGCA ACACCTGCTC GACCGCGACC TTCGTGTCTGA AATTCCCGGC 240
 GTAGACACGG TCGGAAACCA GTTCGACAGA CCCCAGGAGG CACTGGCGCT GGCGCTCGAT 300
 CAGGAACGCA CAGTCACCGA CCAGGTCTGGT CGGCTGACAG CGGTGGCCCC CGACGAGGGC 360
 GATTTCTCTG GCGAGCAGTT CATGCAGTGG TTCTTGACAG AACAGATCTGA AGAGGTGGCC 420
 TTGATGGCAA CCCTGGTGCG GGTGCCGAT CGGGCCGGGG CCAACCTGTT CGAGCTAGAG 480
 AACTTCGTCT CACGTGAAGT GGATGTGGCG CCGGCCGCAT CAGGCGCCCC GCACGCTGCC 540
 GGGGGCCGCC TCTAGATCCC TGGGGGGGAT CAGCGAGTGG TCCCGTTCGC CCGCCCGTCT 600
 TCCAGCCAGG CCTTGGTGCG GCCGGGGTGG TGAGTACCAA TCCAGGCCAC CCCGACCTCC 660
 CGGNAAAAGT CGATGTCCTC GTACTCATCG ACGTTCCAGG AGTACACCGC CCGGCCCTGA 720
 GCTGCCGAGC GGTCAACGAG TTGCGGATAT TCCTTTAACG CAGGCAGTGA GGGTCCCACG 780

GCGGTTGGCC CGACCGCCGT GGCCGCACTG CTGGTCAGGT ATCGGGGGGT CTTGGCGAGC 840
AACAACGTCG GCAGGAGGGG TGGAGCCCCG CGGATCCGCA GACCGGGGGG GCGAAAACGA 900
CATCAACACC GCACGGGATC GATCTGCCGA GGGGGGTGCG GGAATACCGA ACCGGTGTAG 960
GAGCGCCAGC AGTTGTTTTT CCACCAGCGA AGCGTTTTTCG GGTCATCGGN GGCNNTTAAG 1020
T 1021

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG AACGGAAGAA CACAACCATG AAGATGGTGA AATCGATCGC CGCAGGTCTG 60
ACCGCCGCGG CTGCAATCGG CGCCGCTGCG GCCGGTGTGA CTTGATCAT GGCTGGCGGN 120
CCGGTCGTAT ACCAGATGCA GCCGGTCGTC TTCGGCGCGC CACTGCCGTT GGACCCGGNA 180
TCCGCCCTG ANGTCCCGAC CGCCGCCAG TGGACCAGNC TGCTCAACAG NCTCGNCGAT 240
CCCAACGTGT CGTTTGNGAA CAAGGGNAGT CTGGTCGAGG GNGGNATCGG NGGNANCGAG 300
GNGNGNATC GNCGANACA A 321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCCGGTTGGC GACGGTTTTT GGGNGCGGGT GGTAAACCCG CTCGGCCAGC 60
CGATCGACGG GCGCGGAGAC GTCGACTCCG ATACTCGGCG CGCGCTGGAG CTCCAGGCGC 120
CCTCGGTGGT GNACCGGCAA GGCCTGAAGG AGCCGTTGNA GACCGGGATC AAGGCGATTG 180
ACGCGATGAC CCCGATCGGC CGCGGGCAGC GCCAGCTGAT CATCGGGGAC CGCAAGACCG 240
GCAAAAACCG CCGTCTGTGT CGGACACCAT CCTCAAACCA GCGGGAAGAA CTGGGAGTCC 300
GGTGGATCCC AAGAAGCAGG TCGCCTTG TG TATACGTTGG CCATCGGGCA AGAAGGGGAA 360

CTTACCATCG CCG

373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCGT GATGGGATTC CTGGGCGGGG CCGGTCCGCT GGCGGTGGTG GATCAGCAAC	60
TGGTTACCCG GGTGCCGCAA GGCTGGTCGT TTGCTCAGGC AGCCGCTGTG CCGGTGGTGT	120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAAGGCGGGC GAATCGGTGC	180
TGATCCATGC CGGTACCGGC GGTGTGGGCA TGGCGGCTGT GCAGCTGGCT CGCCAGTGGG	240
GCGTGGAGGT TTTCGTCACC GCCAGCCGTG GNAAGTGGGA CACGCTGCGC GCCATNGNGT	300
TTGACGACGA NCCATATCGG NGATTCCNC ACATNCGAAG TTCCGANGGA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG TTCATTCCGT TCGACCAGCG GCTGGCGATA ATCGACGAAG TGATCAAGCC	60
GCGGTTCCGCG GCGCTCATGG GTCACAGCGA GTAATCAGCA AGTTCTCTGG TATATCGCAC	120
CTAGCGTCCA GTTGCTTGCC AGATCGCTTT CGTACCGTCA TCGCATGTAC CCGTTCGCGT	180
GCCGCACGCT CATGCTGGCG GCGTGCATCC TGGCCACGGG TGTGGCGGGT CTCGGGGTCC	240
GCGCGCAGTC CGCAGCCCAA ACCGCGCCGG TGCCCCACTA CTACTGGTGC CCGGGGCAGC	300
CTTTCGACCC CGCATGGGGG CCCAACTGGG ATCCCTACAC CTGCCATGAC GACTTCCACC	360
GCGACAGCGA CGGCCCCGAC CACAGCCGCG ACTACCCCGG ACCCATCCTC GAAGGTCCCG	420
TGCTTGACGA TCCCGGTGCT GCGCCGCCGC CCCC GGCTGC CCGTGGCGGC GCATAGCGCT	480
CGTTGACCGG GCCGCATCAG CGAATACGCG TATAAACCCG GCGTGCCCC CCGCAAGCTA	540
CGACCCCGCG CGGGGCAGAT TTACGCTCCC GTGCCGATGG ATCGCGCCGT CCGATGACAG	600
AAAATAGGCG ACGGTTTTGG CAACCGCTTG GAGGACGCTT GAAGGGAACC TGTCATGAAC	660

GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CCCGCACACC CGTTCGCCCG 720
ATCGTG 726

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG ACGAACGTCG GGCCACCAC CGCCTATGCG TTGATGCAGG CGACCGGGAT 60
GGTCGCCGAC CATATCCAAG CATGCTGGGT GCCCACTGAG CGACCTTTTG ACCAGCCGGG 120
CTGCCCGATG GCGGCCCGGT GAAGTCATTG CGCCGGGGCT TGTGCACCTG ATGAACCCGA 180
ATAGGGAACA ATAGGGGGGT GATTGGCAG TTCAATGTCG GGTATGGCTG GAAATCCAAT 240
GGCGGGGCAT GTCGGCGCC GACCAGGCTC GCGCAGGCGG GCCAGCCCGA ATCTGGAGGG 300
AGCACTCAAT GCGGCGATG AAGCCCCGA CCGGCGACGG TCCTTTGGAA GCAACTAAGG 360
AGGGGCGCGG CATTGTGATG CGAGTACCAC TTGAGGGTGG CGGTGCGCTG GTCGTCGAGC 420
TGACACCCGA CGAAGCCGCC GCACTGGGTG ACGAACTCAA AGGCGTTACT AGCTAAGACC 480
AGCCCAACGG CGAATGGTCG GCGTTACGCG CACACCTTCC GGTAGATGTC CAGTGTCTGC 540
TCGGCGATGT ATGCCCAGGA GAACTCTTGG ATACAGCGCT 580

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CCGGGGGTTT TGGCGGGGCC GGGCGGTCG GCGGCAACGG CGGGGCCGGC 60
GGTACCGCCG GGTTGTTCCG TGTCGGCGGG GCCGGTGGGG CCGGAGGCAA CGGCATCGCC 120
GGTGTACCGG GTACGTCGGC CAGCACACCG GGTGGATCCG 160

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGACA CGCTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCC CGTTCGCGGA GGCGGCTGCC	120
AAGGCGATGG GAATCGACAA GCTGCGGGTA ATTCATACCG GAATGGACCC CGTCGTCGCT	180
GAACGCGAAC AGTGGGACGA CGGCAACAAC ACGTTGGCGT TGGCGCCCGG TGTCGTTGTC	240
GCCTACGAGC GCAACGTACA GACCAACGCC CG	272

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG GTTCTCGGAC TATCTGCGCA CGGTGACGCA GCGCGACGTG CGCGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCCTGCCGC GGTTCATGCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGGTCATCGG GGTCGACGCG GGGACGATCC	180
GTTCGGATCT GGCCTGGTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCC GCCTGGTCGC	240
GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG	300
CGGCCTGGTT GCGCGGG	317

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTCGATGA ACAGCGTTGC CGGACGCGCG GCGGCCAGCA CGTCGGTGTA	60
GCAGCGCCCG ACCACCTCGC CGGTGGGCAG CATGGTGATG ACCACGTCGG CCTCGGCCAC	120
CGCTTCGGGC GCGCTACGAA ACACCGCGAC ACCGTGCGCG GCGGCGCCGG ACGCCGCCGT	180
GG	182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
GATCGCGAAG TTTGGTGAGC AGGTGGTCGA CGCGAAAGTC TGGGCGCCTG CGAAGCGGGT    60
CGGCGTTCAC GAGGCCAAGA CACGCCTGTC CGAGCTGCTG CGGCTCGTCT ACGGCGGGCA    120
GAGGTTGAGA TTGCCCCCGG CGGCGAGCCG GTAGCAAAGC TTGTGCCGCT GCATCCTCAT    180
GAGACTCGGC GGTTAGGCAT TGACCATGGC GTGTACCGCG TGCCCGACGA TTTGGACGCT    240
CCGTTGTCAG ACGACGTGCT CGAACGCTTT CACCGGTGAA GCGCTACCTC ATCGACACCC    300
ACGTTTGG                                     308
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
CCGACGACGA GCAACTCACG TGGATGATGG TCGGCAGCGG CATTGAGGAC GGAGAGAATC    60
CGGCCGAAGC TGCCGCGCGG CAAGTGCTCA TAGTGACCGG CCGTAGAGGG CTCCCCCGAT    120
GGCACCGGAC TATTCTGGTG TGCCGCTGGC CGGTAAGAGC GGGTAAAAGA ATGTGAGGGG    180
ACACGATGAG CAATCACACC TACCGAGTGA TCGAGATCGT CGGGACCTCG CCCGACGGCG    240
TCGACGCGGC AATCCAGGGC GGTCTGG                                     267
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
CTCGTGCCGA AAGAATGTGA GGGGACACGA TGAGCAATCA CACCTACCGA GTGATCGAGA    60
TCGTCGGGAC CTCGCCCGAC GGCCTCGACG CGGCAATCCA GGGCGGTCTG GCGCGAGCTG    120
```

CGCAGACCAT GCGCGCGCTG GACTGGTTTCG AAGTACAGTC AATTCGAGGC CACCTGGTGG	180
ACGGAGCGGT CGCGCACTTC CAGGTGACTA TGAAAGTCGG CTTCCGCTGG AGGATTCTCTG	240
AACCTTCAAG CGCGGCCGAT AACTGAGGTG CATCATTAAG CGACTTTTCC AGAACATCCT	300
GACGCGCTCG AAACGCGGTT CAGCCGACGG TGGCTCCGCC GAGGCGCTGC CTCCAAAATC	360
CCTGCGACAA TTCGTCGGCG GCGCCTACAA GGAAGTCGGT GCTGAATTCTG TCGGGTATCT	420
GGTCGACCTG TGTGGGCTGC AGCCGGACGA AGCGGTGCTC GACGTCGGCT GCGGCTCGGG	480
GCGGATGGCG TTGCCGCTCA CCGGCTATCT GAACAGCGAG GGACGCTACG CCGGCTTCGA	540
TATCTCGCAG AAAGCCATCG CGTGGTGCCA GGAGCACATC ACCTCGGCGC ACCCCAACTT	600
CCAGTTCGAG GTCTCCGACA TCTACAACTC GCTGTACAAC CCGAAAGGGA AATACCAGTC	660
ACTAGACTTT CGCTTTCCAT ATCCGGATGC GTCGTTTCGAT GTGGTGTTTC TTACCTCGGT	720
GTTCACCCAC ATGTTTCCGC CGGACGTGGA GCACTATCTG GACGAGATCT CCCGCGTGCT	780
GAAGCCCGGC GGACGATGCC TGTGCACGTA CTTCTTGCTC AATGACGAGT CGTTAGCCCA	840
CATCGCGGAA GGAAAGAGTG CGCACAACTT CCAGCATGAG GGACCGGGTT ATCGGACAAT	900
CCACAAGAAG CGGCCCCAAG AAGCAATCGG CTTGCCGGAG ACCTTCGTCA GGGATGTCTA	960
TGGCAAGTTC GGCCTCGCCG TGCACGAACC ATTGCACTAC GGCTCATGGA GTGGCCGGGA	1020
ACCACGCCTA AGCTTCCAGG ACATCGTCAT CGCGACCAA ACCGCGAGCT AGGTCCGGCAT	1080
CCGGGAAGCA TCGCGACACC GTGGCGCCGA GCGCCGCTGC CGGCAGGCCG ATTAGGCGGG	1140
CAGATTAGCC CGCCGCGGCT CCCGGCTCCG AGTACGSCGC CCCGAATGGC GTCACCGGCT	1200
GGTAACCACG CTTGCGCGCC TGGGCGGCGG CCTGCCGGAT CAGGTGGTAG ATGCCGACAA	1260
AGCCTGCGTG ATCGGTCATC ACCAACGGTG ACAGCAGCCG GTTGTGCACC AGCGCGAACG	1320
CCACCCCGGT CTCCGGGTCT GTCCAGCCGA TCGAGCCGCC CAAGCCCACA TGACCAAACC	1380
CCGGCATCAC GTTGCCGATC GGCATACCGT GATAGCCAAG ATGAAAATTT AAGGGCACCA	1440
ATAGATTTCTG ATCCGGCAGA ACTTGCCGTC GGTTCGGGT CAGGCCCCGTG ACCAGCTCCC	1500
GCGACAAGAA CCGTATGCCG TCGATCTCGC CTCGTGCCG	1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
CTGCAGGGTG GCGTGGATGA GCGTCACCGC GGGGCAGGCC GAGCTGACCG CCGCCCAGGT      60
CCGGGTTGCT GCGGCGGCCT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT      120
CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC      180
CCCGGCGATC GCGGTCAACG AGGCCGAATA CGGCGAGATG TGGGCCCAAG ACGCCGCCGC      240
GATGTTTGGC TACGCCGCGG CGACGGCGAC GGCGACGGCG ACGTTGCTGC CGTTCGAGGA      300
GGCGCCGGAG ATGACCAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCGG TCGAGGAGGC      360
CTCCGACACC GCCGCGGCGA ACCAGTTGAT GAACAATGTG CCCCAGGCGC TGAAACAGTT      420
GGCCCAGCCC ACGCAGGGCA CCACGCCTTC TTCCAAGCTG GGTGGCCTGT GGAAGACGGT      480
CTCGCCGCAT CGGTCGCCGA TCAGCAACAT GGTGTCGATG GCCAACAACC ACATGTCGAT      540
GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC      600
GGCGGCGGCC GCCCAGGCCG TGCAAACCGC GGCGCAAAAC GGGGTCCGGG CGATGAGCTC      660
GCTGGGCAGC TCGCTGGGTT CTTCCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTCTG      720
GGCGGCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG      780
GAACGGTGGT CCGGCGTAAG GTTTACCCCC GTTTTCTGGA TGCGGTGAAC TTCGTCAACG      840
GAAACAGTTA C                                                    851
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
GATCGATCGG GCGGAAATTT GGACCAGATT CGCCTCCGGC GATAACCCAA TCAATCGAAC      60
CTAGATTTAT TCCGTCCAGG GGCCCGAGTA ATGGCTCGCA GGAGAGGAAC CTTACTGCTG      120
CGGGCACCTG TCGTAGGTCC TCGATACGGC GGAAGGCGTC GACATTTTCC ACCGACACCC      180
CCATCCAAAC GTTCGAGGGC CACTCCAGCT TGTGAGCGAG GCGACGCAGT CGCAGGCTGC      240
GCTTGGTCAA GATC                                                    254
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GATCCTGACC GAAGCGGCCG CCGCCAAGGC GAAGTCGCTG TTGGACCAGG AGGGACGGGA      60
CGATCTGGCG CTGCGGATCG CGGTTTCAGCC GGGGGGGTGC GCTGGATTGC GCTATAACCT      120
TTTCTTCGAC GACCGGACGC TGGATGGTGA CCAAACCGCG GAGTTCGGTG GTGTACAGTT      180
GATCGTGGAC CGGATGAGCG CGCCGTATGT GGAAGGCGCG TCGATCGATT TCGTCGACAC      240
TATTGAGAAG CAAGGTTTAC CATCGACAAT CCCAACGCCA CCGGCTCCTG CGCGTGCGGG      300
GATTCGTTCA ACTGATAAAA CGCTAGTACG ACCCCGCGGT GCGCAACACG TACGAGCACA      360
CCAAGACCTG ACCGCGCTGG AAAAGCAACT GAGCGATGCC TTGCACCTGA CCGCGTGGCG      420
GGCCGCCGGC GGCAGGTGTC ACCTGCATGG TGAACAGCAC CTGGGCCTGA TATTGCGACC      480
AGTACACGAT TTTGTGATC GAGGTCACCT CGACCTGGGA GAACTGCTTG CGGAACGCGT      540
CGCTGCTCAG CTTGGCCAAG GCCTGATCGG AGCGCTTGTC GCGCACGCCG TCGTGGATAC      600
CGCACAGCGC ATTGCGAACG ATGGTGTCCA CATCGCGGTT CTCCAGCGCG TTGAGGTATC      660
CCTGAATCGC GGTTTTGGCC GGTCCCTCCG AGAATGTGCC TGCCGTGTTG GCTCCGTTGG      720
TGCGGACCCC GTATATGATC GCCGCCGTCA TAGCCGACAC CAGCGCGAGG GCTACCACAA      780
TGCCGATCAG CAGCCGCTTG TGCCGTCGCT TCGGGTAGGA CACCTGCGGC GGCACGCCGG      840
GATATGCGGC GGGCGGCAGC GCCGCGTCGT CTGCCGCTCC CGGGGCGAAG GCCGGTTCGG      900
CGGCGCCGAG GTCGTGGGGG TAGTCCAGGG CTTGGGGTTC GTGGGATGAG GGCTCGGGGT      960
ACGGCGCCGG TCCGTTGGTG CCGACACCGG GGTTCGGCGA GTGGGGACCG GGCATTGTGG      1020
TTCTCCTAGG GTGGTGGACG GGACCAGCTG CTAGGGCGAC AACC GCCCGT CGCGTCAGCC      1080
GGCAGCATCG GCAATCAGGT GAGCTCCCTA GGCAGGCTAG CGCAACAGCT GCCGTAGCT      1140
CTCAACGCGA CGGGGCGGGC CGCGGCGCCG ATAATGTTGA AAGACTAGGC AACCTTAGGA      1200
ACGAAGGACG GAGATTTTGT GACGATC                                     1227

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCAACGG CGGGGCCGGC GGGGCCGGCG      60
GGACCGGGCGC TAACGGTGGT GCCGGCGGCA ACGCCTGGTT GTTCGGGGCC GCGGGGTCCG      120
GCGGNGCCGG CACCAATGGT GNGTCGGCG GGTCCGGCGG ATTTGTCTAC GGCAACGGCG      180
G                                                                                   181

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCAACGG CGGTGTCGGC GGCCGGGGCG      60
GCGACGGCGT CTTTGCCGGT GCCGGCGGCC AGGGCGGCCT CGGTGGGCAG GGCGGCAATG      120
GCGGCGGCTC CACCGGCGGC AACGGCGGTC TTGGCGGCGC GGGCGGTGGC GGAGGCAACG      180
CCCCGGACGG CGGCTTCGGT GGCAACGGCG GTAAGGGTGG CCAGGGCGGN ATTGGCGGCG      240
GCACTCAGAG CGCGACCGGC CTCGGNGGTG ACGGCGGTGA CGGCGGTGAC                    290

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GATCCAGTGG CATGGNGGGT GTCAGTGGAA GCAT

```

34

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTGCT CGTCCCCCCC TTGCCGCCGA CGCCACCGGT CCCACCGTTA CCGAACAAGC 60
TGGCGTGGTC GCCAGCACCC CCGGCACCGC CGACGCCGGA GTCGAACAAT GGCACCGTCG 120
TATCCCCACC ATTGCCGCCG GNCCCACCGG CACCG 155

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA CGGGGCGCCG GGGACCGGC AGCCCGGNGG GGCCGGGGGG TGG 53

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCGCG GCGCCACCCC GACCAGCGGC GGCAACGGCG 60
GCACCGGCGG CAACGGCGCG AACGCCACCG TCGTCGGNGG GGCCGGCGGG GCCGGCGGCA 120
AGGGCGGCAA CG 132

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCCGNAGCCA 60
CCNGCCAAGA ATCCTCCGNG TCCNCCAATG GCGCGAATGG CGGACAGGGC GGCAACGGCG 120
GCANCGGCGG CA 132

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCC CGATGCCGGC	120
ATGAACGGGC GGCATCAAAT TAGTGAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCGG	360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCCG GGCCGTCGGA GGGGACAGTT	540
CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCCG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG	660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCCA CG	702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG CGCTGTCGGG CGACGTGGCG GTCAAAGCGG CATCGCTCGG TGGCGGTGGA	60
GGCGGCGGGG TGCCGTCGGC GCCGTTGGGA TCCGCGATCG GGGGCGCCGA ATCGGTGCGG	120
CCCGCTGGCG CTGGTGACAT TGCCGGCTTA GGCCAGGGAA GGGCCGGCGG CGGCGCCGCG	180
CTGGGCGGCG GTGGCATGGG AATGCCGATG GGTGCCGCGC ATCAGGGACA AGGGGGCGCC	240
AAGTCCAAGG GTTCTCAGCA GGAAGACGAG GCGCTCTACA CCGAGGATCC TCGTGCCG	298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1058 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

CGGCACGAGG ATCGAATCGC GTCGCCGGGA GCACAGCGTC GCACTGCACC AGTGGAGGAG      60
CCATGACCTA CTCGCCGGGT AACCCCGGAT ACCCGCAAGC GCAGCCCGCA GGCTCCTACG      120
GAGGCGTCAC ACCCTCGTTC GCCCACGCCG ATGAGGGTGC GAGCAAGCTA CCGATGTACC      180
TGAACATCGC GGTGGCAGTG CTCGGTCTGG CTGCGTACTT CGCCAGCTTC GGCCCAATGT      240
TCACCCCTCAG TACCGAACTC GGGGGGGGTG ATGGCGCAGT GTCCGGTGAC ACTGGGCTGC      300
CGGTCGGGGT GGCTCTGCTG GCTGCGCTGC TTGCCGGGGT GGTTCCTGGT CCTAAGGCCA      360
AGAGCCATGT GACGGTAGTT GCGGTGCTCG GGGTACTCGG CGTATTTCTG ATGGTCTCGG      420
CGACGTTTAA CAAGCCCAGC GCCTATTCGA CCGGTTGGGC ATTGTGGGTT GTGTTGGCTT      480
TCATCGTGTT CCAGGCGGTT GCGGCAGTCC TGGCGCTCTT GGTGGAGACC GGCGCTATCA      540
CCGCGCCGGC GCCGCGGCC AAGTTCGACC CGTATGGACA GTACGGGCGG TACGGGCAGT      600
ACGGGCAGTA CGGGGTGAG CCGGGTGGGT ACTACGGTCA GCAGGGTGCT CAGCAGGCCG      660
CGGGACTGCA GTCGCCCCGC CCGCAGCAGT CTCCGAGCC TCCCGGATAT GGGTCGCAGT      720
ACGGCGGCTA TTCGTCCAGT CCGAGCCAAT CGGGCAGTGG ATACACTGCT CAGCCCCCGG      780
CCCAGCCGCC GGCGCAGTCC GGGTCGCAAC AATCGCACCA GGGCCCATCC ACGCCACCTA      840
CCGGCTTTCC GAGCTTCAGC CCACCACCAC CGGTCAGTGC CGGGACGGGG TCGCAGGCTG      900
GTTGGGCTCC AGTCAACTAT TCAAACCCCA GCGGGGGCGA GCAGTCGTCG TCCCCCGGGG      960
GGGCGCCGGT CTAACCGGGC GTTCCCGCGT CCGGTCGCGC GTGTGCGCGA AGAGTGAACA     1020
GGGTGTCAGC AAGCGCGGAC GATCCTCGTG CCGAATTC                               1058

```

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

CGGCACGAGA GACCGATGCC GCTACCCTCG CGCAGGAGGC AGGTAATTTC GAGCGGATCT      60
CCGGCGACCT GAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGGTTTC TTGCAGGGCC      120

```

AGTGGCGCGG CGCGGCGGGG ACGGCCGCCC AGGCCGCGGT GGTGCGCTTC CAAGAAGCAG 180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCCGCGCTCC 240
AATACTCGAG GGCCGACGAG GAGCAGCAGC AGGCGCTGTC CTCGCAAATG GGCTTCTGAC 300
CCGCTAATAC GAAAAGAAAC GGAGCAA 327

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA 60
CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTCT 120
TCTTCATCAG GAAGTCACA CCGGCCACCC TGCCCTCGGN TACCTTTTCGG 170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG 60
CCGGGGGTGG CGGCGGAACC GGTGGGTTGC TCTTCGGCAA CGGCGGTGCC GGCGGGCACG 120
GGGCCGT 127

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA 60
CGGCGGCTCC GGCCTCAACG G 81

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG      60
GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG      120
GAAACGGTGG TGCCGGTGGG CTGATCTGG      149
```

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCG      60
ACGCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT      120
TCGAAGTACA GTCAATTCTGA GGCCACCTGG TCGACGGAGC GGTCGCGCAC TTCCAGGTGA      180
CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA      240
GGTGCATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTCGAAACGC GGTTCAGCCG      300
ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTCTGC GGCGG      355
```

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA      60
CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG      120
CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG      180
CCGCGGTCTG CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG      240
```

```

GCCGCCGCCA ACACGCCGAA TGCCAGCCG GCGATCCCA ACGCAGCACC TCCGCCGGCC      300
GACCCGAACG CACCGCCGCC ACCTGTCATT GCCCCAAACG CACCCCAACC TGTCCGGATC      360
GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC      420
GCCCCACTTCG ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCC      480
GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAG      540
CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG      600
GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC      660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG      720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC      780
GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG      840
GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG      900
GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCGG CCGGGGAAGT CGCTCCTACC      960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA                          999

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1           5           10           15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20           25           30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35           40           45

Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50           55           60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65           70           75           80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85           90           95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro

```

100	105	110
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser 115 120 125		
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp 130 135 140		
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro 145 150 155 160		
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg 165 170 175		
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala 180 185 190		
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro 195 200 205		
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val 210 215 220		
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys 225 230 235 240		
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn 245 250 255		
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly 260 265 270		
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu 275 280 285		
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro 290 295 300		
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr 305 310 315 320		
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala 325 330		

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

1	5	10	15
Val	Ala	Ala	Leu
	20		

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10						15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
 1 5 10 15

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Cys Gly Asp Arg Ser Gly Gly Asn Leu Asp Gln Ile Arg Leu Arg
 1 5 10 15

Arg Asp Arg Ser Gly Gly Asn Leu
 20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15

Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30

Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45

Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60

Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65 70 75 80

Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95

Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
 100 105 110

Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125

Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
 130 135 140

Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160

Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175

Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 5 10 15

Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
 20 25 30

Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 35 40 45

Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
 50 55 60

Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
 65 70 75 80

Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
 85 90 95

Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
 100 105 110

Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
 115 120 125

Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
 130 135 140

Thr Gly Gly Pro
 145

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1           5           10           15
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
20           25           30
Gln Arg Asp Ala Leu Cys Leu Ser Thr Gln Ile Ser Arg Gln Ser
35           40           45
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
50           55           60
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
65           70           75           80
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
85           90           95
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
100          105          110
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
115          120          125
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
130          135          140
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
145          150          155          160
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
165          170          175
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
180          185          190
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
195          200          205
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
210          215          220
Phe Pro Ile Val Ala Arg
225          230

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
          20           25           30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
          35           40           45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
          50           55           60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
          65           70           75           80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
          85           90           95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
          100          105          110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
          115          120          125

Gly Pro Pro Ala
          130

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1           5           10           15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Leu Ser Asn Pro Pro
          20           25           30

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
          35           40           45

```

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50 55 60

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65 70 75 80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85 90 95

Ser Glu Arg Lys
100

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1 5 10 15

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20 25 30

Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35 40 45

Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50 55 60

Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65 70 75 80

Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85 90 95

Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100 105 110

Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115 120 125

Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130 135 140

His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145 150 155 160

Asp Arg Arg

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
 1             5             10             15

Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
 20             25             30

Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
 35             40             45

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
 50             55             60

Arg Gly Arg Lys Glu Ala Val Ala Ala Val Ala Ala Ser Leu Arg
 65             70             75             80

Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
 85             90             95

Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100            105            110

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
115            120            125

Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
130            135            140

Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
145            150            155            160

Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
165            170            175

Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
180            185            190

His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
195            200            205

Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
210            215            220

Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
225            230            235            240

```


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Asp	Asp	Pro	Asp	Met	Pro	Gly	Thr	Val	Ala	Lys	Ala	Val	Ala	Asp	Ala
1			5					10					15		
Leu	Gly	Arg	Gly	Ile	Ala	Pro	Val	Glu	Asp	Ile	Gln	Asp	Cys	Val	Glu
			20					25					30		
Ala	Arg	Leu	Gly	Glu	Ala	Gly	Leu	Asp	Asp	Val	Ala	Arg	Val	Tyr	Ile
		35					40					45			
Ile	Tyr	Arg	Gln	Arg	Arg	Ala	Glu	Leu	Arg	Thr	Ala	Lys	Ala	Leu	Leu
	50					55					60				
Gly	Val	Arg	Asp	Glu	Leu	Lys	Leu	Ser	Leu	Ala	Ala	Val	Thr	Val	Leu
65					70					75					80
Arg	Glu	Arg	Tyr	Leu	Leu	His	Asp	Glu	Gln	Gly	Arg	Pro	Ala	Glu	Ser
				85					90					95	
Thr	Gly	Glu	Leu	Met	Asp	Arg	Ser	Ala	Arg	Cys	Val	Ala	Ala	Ala	Glu
			100					105					110		
Asp	Gln	Tyr	Glu	Pro	Gly	Ser	Ser	Arg	Arg	Trp	Ala	Glu	Arg	Phe	Ala
		115					120					125			

Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140

Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160

Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
 165 170 175

Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190

Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205

Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220

Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240

His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255

Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 260 265 270

Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285

Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300

Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320

Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335

Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350

Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365

Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380

Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400

Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415

Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
 435 440 445
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
 465 470 475 480
 Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
 1 5 10 15
 Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
 20 25 30
 Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
 35 40 45
 Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
 50 55 60
 Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
 65 70 75 80
 Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
 85 90 95
 Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
 100 105 110
 Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
 115 120 125
 Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
 130 135 140
 Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
 145 150 155 160

Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
 165 170 175

Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
 180 185 190

Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
 195 200 205

Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
 210 215 220

Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
 225 230 235 240

Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
 245 250 255

Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
 260 265

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
 1 5 10 15

Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
 20 25 30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
 35 40 45

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60

Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80

Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95

Gln

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gly	Ala	Ala	Val	Ser	Leu	Leu	Ala	Ala	Gly	Thr	Leu	Val	Leu	Thr	Ala	1	5	10	15
Cys	Gly	Gly	Gly	Thr	Asn	Ser	Ser	Ser	Ser	Gly	Ala	Gly	Gly	Thr	Ser	20	25	30	
Gly	Ser	Val	His	Cys	Gly	Gly	Lys	Lys	Glu	Leu	His	Ser	Ser	Gly	Ser	35	40	45	
Thr	Ala	Gln	Glu	Asn	Ala	Met	Glu	Gln	Phe	Val	Tyr	Ala	Tyr	Val	Arg	50	55	60	
Ser	Cys	Pro	Gly	Tyr	Thr	Leu	Asp	Tyr	Asn	Ala	Asn	Gly	Ser	Gly	Ala	65	70	75	80
Gly	Val	Thr	Gln	Phe	Leu	Asn	Asn	Glu	Thr	Asp	Phe	Ala	Gly	Ser	Asp	85	90	95	
Val	Pro	Leu	Asn	Pro	Ser	Thr	Gly	Gln	Pro	Asp	Arg	Ser	Ala	Glu	Arg	100	105	110	
Cys	Gly	Ser	Pro	Ala	Trp	Asp	Leu	Pro	Thr	Val	Phe	Gly	Pro	Ile	Ala	115	120	125	
Ile	Thr	Tyr	Asn	Ile	Lys	Gly	Val	Ser	Thr	Leu	Asn	Leu	Asp	Gly	Pro	130	135	140	
Thr	Thr	Ala	Lys	Ile	Phe	Asn	Gly	Thr	Ile	Thr	Val	Trp	Asn	Asp	Pro	145	150	155	160
Gln	Ile	Gln	Ala	Leu	Asn	Ser	Gly	Thr	Asp	Leu	Pro	Pro	Thr	Pro	Ile	165	170	175	
Ser	Val	Ile	Phe	Arg	Ser	Asp	Lys	Ser	Gly	Thr	Ser	Asp	Asn	Phe	Gln	180	185	190	
Lys	Tyr	Leu	Asp	Gly	Val	Ser	Asn	Gly	Ala	Trp	Gly	Lys	Gly	Ala	Ser	195	200	205	
Glu	Thr	Phe	Ser	Gly	Gly	Val	Gly	Val	Gly	Ala	Ser	Gly	Asn	Asn	Gly	210	215	220	
Thr	Ser	Ala	Leu	Leu	Gln	Thr	Thr	Asp	Gly	Ser	Ile	Thr	Tyr	Asn	Glu	225	230	235	240
Trp	Ser	Phe	Ala	Val	Gly	Lys	Gln	Leu	Asn	Met	Ala	Gln	Ile	Ile	Thr	245	250	255	

Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
 290 295 300
 Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
 305 310 315 320
 Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
 325 330 335
 Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
 340 345 350
 Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15
 Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60
 Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125

Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140

Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160

Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175

Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190

Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205

Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220

Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240

Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255

Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270

His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285

Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300

Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15

Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30

Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45

Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys
 305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335
 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp

340	345	350
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser 355 360 365		
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile 370 375 380		
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser 385 390 395 400		
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn 405 410 415		
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn 420 425 430		
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn 435 440 445		
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly 450 455 460		
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile 465 470 475 480		
Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly 485 490 495		
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu 500 505 510		
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val 515 520 525		
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu 530 535 540		
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr 545 550 555 560		
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly 565 570 575		
Lys Ala Glu Gln 580		

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1           5           10           15

Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
          20           25           30

Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
          35           40           45

Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
          50           55           60

Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
65           70           75           80

Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
          85           90           95

Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
          100          105          110

Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
          115          120          125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
          130          135          140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
          145          150          155          160

Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
          165          170          175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
          180          185          190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
          195          200          205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
          210          215          220

Lys Trp Asn Glu Pro Val Asn Val Asp
          225          230

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1           5           10           15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
          20           25           30
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
          35           40           45
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
          50           55           60
Pro Arg
          65

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1           5           10           15
Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
          20           25           30
Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
          35           40           45
Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
          50           55           60
Ser Pro Pro Leu Pro
          65

```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1           5           10           15

```

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp

305		310		315		320									
Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Asn	Trp	Gln
			325						330					335	
Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly
			340					345						350	
Pro	Pro	Ala													
		355													

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Ser	Pro	Lys	Pro	Asp	Ala	Glu	Glu	Gln	Gly	Val	Pro	Val	Ser	Pro	Thr
1			5						10					15	
Ala	Ser	Asp	Pro	Ala	Leu	Leu	Ala	Glu	Ile	Arg	Gln	Ser	Leu	Asp	Ala
			20					25					30		
Thr	Lys	Gly	Leu	Thr	Ser	Val	His	Val	Ala	Val	Arg	Thr	Thr	Gly	Lys
		35					40					45			
Val	Asp	Ser	Leu	Leu	Gly	Ile	Thr	Ser	Ala	Asp	Val	Asp	Val	Arg	Ala
	50				55						60				
Asn	Pro	Leu	Ala	Ala	Lys	Gly	Val	Cys	Thr	Tyr	Asn	Asp	Glu	Gln	Gly
65					70					75				80	
Val	Pro	Phe	Arg	Val	Gln	Gly	Asp	Asn	Ile	Ser	Val	Lys	Leu	Phe	Asp
			85						90					95	
Asp	Trp	Ser	Asn	Leu	Gly	Ser	Ile	Ser	Glu	Leu	Ser	Thr	Ser	Arg	Val
			100					105						110	
Leu	Asp	Pro	Ala	Ala	Gly	Val	Thr	Gln	Leu	Leu	Ser	Gly	Val	Thr	Asn
			115				120					125			
Leu	Gln	Ala	Gln	Gly	Thr	Glu	Val	Ile	Asp	Gly	Ile	Ser	Thr	Thr	Lys
		130				135					140				
Ile	Thr	Gly	Thr	Ile	Pro	Ala	Ser	Ser	Val	Lys	Met	Leu	Asp	Pro	Gly
145					150					155				160	
Ala	Lys	Ser	Ala	Arg	Pro	Ala	Thr	Val	Trp	Ile	Ala	Gln	Asp	Gly	Ser
				165					170					175	
His	His	Leu	Val	Arg	Ala	Ser	Ile	Asp	Leu	Gly	Ser	Gly	Ser	Ile	Gln

180	185	190
Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp		
195	200	205

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val		
1	5	10
Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln		
20	25	30
His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val		
35	40	45
Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu		
50	55	60
Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe		
65	70	75
Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu		
85	90	95
Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala		
100	105	110
Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val		
115	120	125
Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp		
130	135	140
Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn		
145	150	155
Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg		
165	170	175
Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly		
180	185	190
Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile		
195	200	205
Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe		

210	215	220
Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp		
225	230	235 240
Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg		
	245	250 255
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln		
	260	265 270
Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys		
	275	280 285

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr		
1	5	10 15
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp		
	20	25 30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg		
	35	40 45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg		
	50	55 60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro		
65	70	75 80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp		
	85	90 95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu		
	100	105 110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val		
	115	120 125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn		
	130	135 140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro		
145	150	155 160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu		

165

170

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
 1             5             10             15
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
 20             25             30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
 35             40             45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
 50             55             60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
 65             70             75             80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
 85             90             95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
 100            105

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
 1             5             10             15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
 20             25             30
Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
 35             40             45
Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 50             55             60
Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr

```


65		70		75		80									
Gly	Lys	Asn	Arg	Arg	Leu	Cys	Arg	Thr	Pro	Ser	Ser	Asn	Gln	Arg	Glu
			85						90					95	
Glu	Leu	Gly	Val	Arg	Trp	Ile	Pro	Arg	Ser	Arg	Cys	Ala	Cys	Val	Tyr
		100					105						110		
Val	Gly	His	Arg	Ala	Arg	Arg	Gly	Thr	Tyr	His	Arg	Arg			
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys	Asp	Ala	Val	Met	Gly	Phe	Leu	Gly	Gly	Ala	Gly	Pro	Leu	Ala	Val
1			5						10					15	
Val	Asp	Gln	Gln	Leu	Val	Thr	Arg	Val	Pro	Gln	Gly	Trp	Ser	Phe	Ala
		20					25						30		
Gln	Ala	Ala	Ala	Val	Pro	Val	Val	Phe	Leu	Thr	Ala	Trp	Tyr	Gly	Leu
		35				40						45			
Ala	Asp	Leu	Ala	Glu	Ile	Lys	Ala	Gly	Glu	Ser	Val	Leu	Ile	His	Ala
	50					55					60				
Gly	Thr	Gly	Gly	Val	Gly	Met	Ala	Ala	Val	Gln	Leu	Ala	Arg	Gln	Trp
65				70						75				80	
Gly	Val	Glu	Val	Phe	Val	Thr	Ala	Ser	Arg	Gly	Lys	Trp	Asp	Thr	Leu
			85						90					95	
Arg	Ala	Xaa	Xaa	Phe	Asp	Asp	Xaa	Pro	Tyr	Arg	Xaa	Phe	Pro	His	Xaa
		100						105						110	
Arg	Ser	Ser	Xaa	Gly											
		115													

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
 1 5 10 15
 Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
 20 25 30
 Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
 35 40 45
 Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
 50 55 60
 His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
 65 70 75 80
 Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
 85 90 95
 Pro Ala Ala Gly Gly Gly Ala
 100

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
 1 5 10 15
 Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
 20 25 30
 Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
 35 40 45
 Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
 50 55 60
 Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
 65 70 75 80
 Asp Glu Leu Lys Gly Val Thr Ser
 85

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1           5           10           15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20           25           30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35           40           45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50           55           60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65           70           75           80
Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85           90           95

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1           5           10           15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20           25           30
Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35           40           45
Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50           55           60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65           70           75           80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85           90           95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100          105          110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115          120          125

```

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
 130 135 140

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
 145 150 155 160

Leu Thr Leu Gln Gly Asp
 165

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg Ala Glu Arg Met
 1 5

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1 5 10 15

Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 20 25 30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 35 40 45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 50 55 60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65 70 75 80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85 90 95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 100 105 110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met

115	120	125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly		
130	135	140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro		
145	150	155
		160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met		
	165	170
		175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met		
	180	185
		190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala		
195	200	205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly		
210	215	220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala		
225	230	235
		240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly		
	245	250
		255
Arg Arg Asn Gly Gly Pro Ala		
260		

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
1	5	10
		15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
20	25	30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
35	40	45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
50	55	60
Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75
		80
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val		

85	90	95
Pro Lys Ala Lys Ser His Val Thr	Val Val Ala Val Leu Gly Val Leu	
100	105	110
Gly Val Phe Leu Met Val Ser Ala Thr	Phe Asn Lys Pro Ser Ala Tyr	
115	120	125
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln		
130	135	140
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr		
145	150	155
Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg		
165	170	175
Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly		
180	185	190
Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln		
195	200	205
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser		
210	215	220
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala		
225	230	235
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser		
245	250	255
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser		
260	265	270
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn		
275	280	285
Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val		
290	295	300

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAGATGG TGAAATCGAT CGCCGCAGGT CTGACCGCCG CGGCTGCAAT CGGCGCCGCT	60
GCGGCCCGGTG TGACTTCGAT CATGGCTGGC GGCCCGGTGG TATACCAGAT GCAGCCGGTC	120

```

GTCTTCGGCG CGCCACTGCC GTTGGACCCG GCATCCGCCC CTGACGTCCC GACCGCCGCC      180
CAGTTGACCA GCCTGCTCAA CAGCCTCGCC GATCCCAACG TGTCGTTTGC GAACAAGGGC      240
AGTCTGGTCG AGGGCGGCAT CGGGGGCACC GAGGCGCGCA TCGCCGACCA CAAGCTGAAG      300
AAGGCCGCCG AGCACGGGGA TCTGCCGCTG TCGTTCAGCG TGACGAACAT CCAGCCGGCG      360
GCCGCCGGTT CGGCCACCGC CGACGTTTCC GTCTCGGGTC CGAAGCTCTC GTCGCCGGTC      420
ACGCAGAACG TCACGTTCTG GAATCAAGGC GGCTGGATGC TGTACGCGC ATCGGCGATG      480
GAGTTGCTGC AGGCCGCAGG GAACTGA                                           507

```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
1           5           10           15

Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
20           25           30

Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
35           40           45

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
50           55           60

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
65           70           75           80

Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
85           90           95

His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
100          105          110

Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
115          120          125

Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
130          135          140

Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
145          150          155          160

```


Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
 85 90 95

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA 60
 AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA 120
 GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC 154

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1 5 10 15
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGTCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT 60
 TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTTCCAGAAC ATCCTGACGC 120

GCTCGAAACG CGGCACAGCC GACGGTGGCT CCGNCGAGGC GCTGNTCCA AAATCCCTGA 180
GACAATTCGN CGGGGGCGCC TACAAGGAAG TCGGTGCTGA ATTCGNCGNG TATCTGGTCG 240
ACCTGTGTGG TCTGNAGCCG GACGAAGCGG TGCTCGACGT CG 282

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT 60
GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC 120
TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA 180
TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT 240
GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG 300
CTCGTATGCG GCCACTGAAG TCGCCAATGC GGCGGCGGCC AGCTAAGCCA GGAACAGTCG 360
GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGA TTTGCGGGCG TTACCACCGG 420
AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCCGC CTCGCTGGTG GCCGCGGCTC 480
AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCCGCCGC GTCGGCGTTT CAGTCGGTGG 540
TCTGGGGTCT GACGGTGGGG TCGTGGATAG GTTCGTGGGC GGGTCTGATG GTGGCGGCGG 600
CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCCC 660
AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCCGG 720
TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA 780
ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG 840
CCGCGATGTT TGGCTACGCC GCGGCGACGG CGACGGCGAC GGCGACGTTG CTGCCGTTCTG 900
AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG 960
AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC 1020
AGCTGGCCCA GCCACGCAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA 1080
CGGTCTCGCC GCATCGGTCTG CCGATCAGCA ACATGGTGTC GATGGCCAAC AACCACATGT 1140

CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTG AAGGGCTTTG	1200
CTCCGGCGGC GGCCGCCAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA	1260
GCTCGCTGGG CAGCTCGCTG GGTTCCTCGG GTCTGGGCGG TGGGGTGGCC GCCAACTTGG	1320
GTCCGGCGGC CTCGGTGGT TCGTTGTCGG TGCCGCAGGC CTGGGCCGCG GCCAACCAGG	1380
CAGTCACCCC GGCGGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG	1440
GGCCCGGGCA GATGCTGGGG GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGGTGGTG	1500
GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG	1560
CCGGCTAGGA GAGGGGGCGC AGACTGTGCT TATTTGACCA GTGATCGGCG GTCTCGGTGT	1620
TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG	1680
GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG	1740
GGACATGGCG GGCCGTTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT	1800
GTGGGCGTCC GCGCAAAACA TTTCCGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC	1860
GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG	1920
GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA	1980
GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA	2040
ACAGGTTCGA TGACCATCAA CTATCAATTC GGGGATGTCG ACGCTCACGG CGCCATGATC	2100
CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTGCTGA TGTGTTGACC	2160
GCGAGTGA CT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTTCAT TACCCAGTTG	2220
GGCCGTAACT TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT	2280
GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTGCGCT CCAGCTGGGC CTGACACCAG	2340
GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT	2400
CTAAGTGGTC AGTGCTGGGG TGTTGGTGGT TTGCTGCTTG GCGGGTTCTT CGGTGCTGGT	2460
CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTCGATCCA	2520
TTCGTCGTGT TGTTGCGGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG	2580
GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT	2640
GTTGGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT	2700
GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC	2760
CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG	2820

GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTTCCTGCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
 GGCCTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG 3000
 GAAGAACGCC AGCCAGCCGG CCCCCTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160
 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175
 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG 60
 ACGTCCCTCG GCGTGTGCGC GGCCTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA 120
 ATTCGTTGA AGTGCCTGCG AGGTATAGGA CTTACAGATT GGTAAATGTA GCGTTCACCC 180

CGTGTGGGG TCGATTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG	240
GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA	300
ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG	360
CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCCGAG CCGTGCCGAC	420
GACTGGGGTG GTGCCCCCGG CTGCCGACGA GGTGTGCTG CTGCTTGCCA CACAATTCCG	480
TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT	540
TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT	600
GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATTT	660
CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGGCCCGG GTTCGGCCTC	720
GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC	780
GGCGTTTCAG TCGGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGTT CGTCGGCGGG	840
TCTGATGGCG GCGGCGGCCT CGCCGTATGT GGCCTGGATG AGCGTCACCG CGGGGCAGGC	900
CCAGCTGACC GCCGCCCAGG TCCGGGTTGC TGCGGCGGCC TACGAGACAG CGTATAGGCT	960
GACGGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCGAA CTGATGACGC TGACCGCGAC	1020
CAACCTCTTG GGGCAAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT	1080
GTGGGGCCAA GACGCGGAGG CGATGTATGG CTACGCCGCC ACGGCGGCGA CGGCGACCGA	1140
GGCGTTGCTG CCGTTCGAGG ACGCCCACT GATCACCAC CCGGCGGGC TCCTTGAGCA	1200
GGCCGTCGCG GTCGAGGAGG CCATCGACAC CGCCGCGCG AACCAGTTGA TGAACAATGT	1260
GCCCCAAGCG CTGCAACAGC TGGCCAGCC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT	1320
GGGTGGGCTG TGGACGGCGG TCTCGCCGA TCTGTCGCC CTCAGCAACG TCAGTTCGAT	1380
AGCCAACAAC CACATGTGCA TGATGGGCAC GGGTGTGTG ATGACCAACA CTTGCACTC	1440
GATGTTGAAG GGCTTAGCTC CGGCGCGGC TCAGGCCGTG GAAACCGCG CGGAAAACGG	1500
GGTCTGGGCG ATGAGCTCGC TGGGCAGCCA GCTGGGTTG TCGCTGGGTT CTTGCGGTCT	1560
GGGCGCTGGG GTGGCCGCCA ACTTGGGTG GCGGCGCTG GTCGGTTCGT TGTCGGTGCC	1620
GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCCGGC GCGCGGGCGC TGCCGCTGAC	1680
CAGCCTGACC AGCGCCGCCC AAACCGCCCC CGGACACATG CTGGG	1725

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

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Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
          20           25           30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
          35           40           45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
          50           55           60
Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65           70           75           80
Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
          85           90           95
Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
          100          105          110
Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
          115          120          125
Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
          130          135          140
Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145          150          155          160
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
          165          170          175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
          180          185          190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
          195          200          205
Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
          210          215          220
Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
225          230          235          240
Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
          245          250          255

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Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335
 Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350
 Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AGTTCAGTCG AGAATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCCAC 60
 CGTCGGACGC GGGGACATCG CAAGCCGACG CGATGGCGTT GGCCGCCGAA GCCGAAGCCG 120
 CCGAAGCCGA AGCGCTGGCC GCCGCGGCGC GGGCCCGTGC CCGTGCCGCC CGGTTGAAGC 180
 GTGAGGCGCT GGCGATGGCC CCAGCCGAGG ACGAGAACGT CCCCAGGAT ATGCAGACTG 240
 GGAAGACGCC GAAGACTATG ACGACTATGA CGACTATGAG GCCGCAGACC AGGAGGCCGC 300
 ACGGTCGGCA TCCTGGCGAC GGC GGTTGCG GGTGCGGTTA CCAAGACTGT CCACGATTGC 360
 CATGGCGGCC GCAGTCGTCA TCATCTGCGG CTTACCCGGG CTCAGCGGAT ACATTGTGTG 420
 GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGCCGCG GCGTTCGCCG CCGGAGCCAA 480
 GCAAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAAGAAG ACGTCGCGCG 540
 TGTGATCGAC AGCTCCACCG GCGAATTCAG GGATGACTTC CAGCAGCGGG CAGCCGATTT 600
 CACCAAGGTT GTCGAACAGT CCAAAGTGGT CACCGAAGGC ACGGTGAACG CGACAGCCGT 660
 CGAATCCATG AACGAGCATT CCGCCGTGGT GTCGTCGCG GCGACTTCAC GGGTCACCAA 720

TTCCGCTGGG GCGAAAGACG AACCACGTGC GTGGCGGCTC AAAGTGACCG TGACCGAAGA	780
GGGGGGACAG TACAAGATGT CGAAAGTTGA GTTCGTACCG TGACCGATGA CGTACGCGAC	840
GTCAACACCG AAACCACTGA CGCCACCGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA	900
GCCGGTGATT CGGCGACCGA GGCATTTGAC ACCGACTCTG CAACGGAATC TACCGCGCAG	960
AAGGGTCAGC GGCACCGTGA CCTGTGGCGA ATGCAGGTTA CCTTGAAACC CGTTCCGGTG	1020
ATTCTCATCC TGCTCATGTT GATCTCTGGG GGCGCGACGG GATGGCTATA CCTTGAGCAA	1080
TACGACCCGA TCAGCAGACG GACTCCGGCG CCGCCCGTGC TGCCGTCGCC GCGGCGTCTG	1140
ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTCG ACCAAGACTT CGCTACCGCC	1200
AGGTCGCACC TCGCCGGCGA TTTCCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG	1260
CTCCGGCGGC CAAACAGAAG TCACTGAAAA CCACCGCCAA GGTGGTGCGC GCGGCCGTGT	1320
CGGAGCTACA TCCGATTTCG GCCGTCGTTT TGGTTTTTGT CGACCAGAGC ACTACCAGTA	1380
AGGACAGCCC CAATCCGTCG ATGGCGGCCA GCAGCGTGAT GGTGACCCTA GCCAAGGTCG	1440
ACGGCAATTG GCTGATCACC AAGTTCACCC CGGTTTAGGT TGCCGTAGGC GGTGCGCAAG	1500
TCTGACGGGG GCGCGGGTGG CTGCTCGTGC GAGATACCGG CCGTTCTCCG GACAATCACG	1560
GCCCCGACCTC AAACAGATCT CGGCCGCTGT CTAATCGGCC GGGTTATTTA AGATTAGTTG	1620
CCACTGTATT TACCTGATGT TCAGATTGTT CAGCTGGATT TAGCTTCGCG GCAGGGCGGC	1680
TGGTGCACTT TGCATCTGGG GTTGTGACTA CTTGAGAGAA TTTGACCTGT TGCCGACGTT	1740
GTTTGTCTGC CATCATTGGT GCTAGTTATG GCCGAGCGGA AGGATTATCG AAGTGGTGGA	1800
CTTCGGGGCG TTACCACCGG AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC	1860
CTCGCTGGTG GCCGCCGCGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC	1920
GTCGGCGTTT CAGTCGGTGG TCTGGGTCTT GACGACGGGA TCGTGGATAG GTTCGTCGGC	1980
GGGTCTGATG GTGGCGGCGG CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA	2040
GGCCGAGCTG ACCGCCGCCC AGGTCCGGGT TGCTCGGGCG GCCTACGAGA CGGCGTATGG	2100
GCTGACGGTG CCCCCGCCGG TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC	2160
GACCAACCTC TTGGGGCAAA ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA	2220
GATGTGGGCC CAAGACGCCG CCGCGATGTT TGGCTACGCC GCCACGGCGG CGACGGCGAC	2280
CGAGGCCTTG CTGCCGTTTC AGGACGCCCC ACTGATCACC AACCCCGGCG GGCTCCTTGA	2340
GCAGGCCCTC GCGGTGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA	2400

TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCCAGGAAA AGCATCTGGC CGTTCGACCA 2460
 ACTGAGTGAA CTCTGGAAAG CCATCTCGCC GCATCTGTCG CCGCTCAGCA ACATCGTGTC 2520
 GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA 2580
 CTCAATGTTG AAGGGCTTTG CTCGGCGGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA 2640
 CGGGGTCCAG GCGATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG 2700
 TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTGCGT 2760
 GCCGCAGGCC TGGGCGCGCG CCAACCAGGC GGTCAACCCG GCGGCGCGGG CGCTGCCGCT 2820
 GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCCAGACAC ATGCTGGGCG GGCTACCGCT 2880
 GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGCGT TCGGGATGCC 2940
 GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCAGCAA 3000
 TCGGGGCCCT CTATGCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly

115	120	125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met		
130	135	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala		
145	150	155 160
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr		
165	170	175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile		
180	185	190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu		
195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu		
210	215	220
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn		
225	230	235 240
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val		
245	250	255
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala		
260	265	270
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met		
275	280	285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu		
290	295	300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser		
305	310	315 320
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro		
325	330	335
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr		
340	345	350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn		
355	360	365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro		
370	375	380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly		
385	390	395

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCAGC	60
GCTGATGGCC GCGCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240
GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC	300
GGCATAACCC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT	360
CACCCAGGCC GTCCTTACGG CCACCAACTT CTCGGTATC AACACGATCC CGATCGCGTT	420
GACCGAGATG GATTATTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA	480
CCAGGCCGAG ACCCGGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT	540
TGATCCCCGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG	600
CTCAACACCG GTTGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA	660
GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTGCAG CAGGTGACGT CGTTGTTCAG	720
CCAGGTGGGC GGCACCGGC GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT	780
GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG	840
CGCGGGCCTG CTGCGCGCG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC	900
GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC	960
CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC	1020
GCAATCCGGC GGCTCCACCA GGCCGGGTCT GGTGCGGCCG GCACCGCTCG CGCAGGAGCG	1080
TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC	1140
AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC ATTTTGCGCA GGAAGGTAAA	1200
GAGAGAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGCTACCCCT CGCGCAGGAG	1260
GCAGGTAATT TCGAGCGGAT CTCGCGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG	1320
ACGGCAGGTT CGTTGCAGGG CCACTGGCGC GGCGCGGCGG GGACGGCCGC CCAGGCCGCG	1380
GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG	1440

AATATTCGTC AGGCCGGCGT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG 1500
 TCCTCGCAAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG 1560
 AGCAGCAGTG GAATTTTCGCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT 1616

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CTTTCTGTGT TGACATTTTG 60
 GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TGGCTGCCA TATCGTCCGG 120
 AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCTAG TCGGCCGCCA TGACAACCTC 180
 TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTCGAACTC 240
 GCCCGATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA 300
 GTGACGTTGC CTTCCGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG 360
 TTCTGCAGCG CGTTGTTTCTG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACCCTGG 420
 TACGCCTCCG AA 432

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met
 1 5 10 15
 Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln
 20 25 30
 Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg
 35 40 45
 Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
 50 55 60

Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr
 65 70 75 80
 Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Tyr
 85 90 95
 Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn
 100 105 110
 His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
 115 120 125
 Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp
 130 135 140
 Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp

355

360

365

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1             5             10             15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
          20             25             30

Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
          35             40             45

Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50             55             60

Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
65             70             75             80

Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser
          85             90             95

Gln Met Gly Phe
          100

```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA      60
GGGCCAGTGG CGCGGC GCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA      120
AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG      180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCTCTCGC AAATGGGCTT      240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTC      300
GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC      360

```

CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA

396

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala
1           5           10           15

Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
20           25           30

Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
35           40           45

Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
50           55           60

Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

GTGGATCCCG ATCCCGTGTT TCGCTATTCT ACGCGAACTC GCGGTTGCCC TATGCGAACA      60
TCCCAAGTAC GTTGCTTCG GTCGAAGCCA TTGCCTGACC GGCTTCGCTG ATCGTCCGCG      120
CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC      180
CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT      240
TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTC CTGGATTGCG CTTGCCGCGG      300
CCTCGATAAC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTTGCTCCGT TTCTTTTCGT      360
ATTAGCGGGT CAGAAGCCCA TTTGCGA                                     387

```

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CGGCACGAGG ATCTCGGTTG GCCCAACGGC GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC	60
TGCGCGCCCG ATGCTTCCTC TGCCCGCAGC CGCGCCTGGA TGGATGGACC AGTTGCTACC	120
TTCCCGACGT TTCGTTCCGT GTCTGTGCGA TAGCGGTGAC CCCGGCGCGC ACGTCGGGAG	180
TGTTGGGGGG CAGGCCGGGT CGGTGGTTTCG GCCGGGGACG CAGACGGTCT GGACGGAACG	240
GGCGGGGGTT CGCCGATTGG CATCTTTGCC CA	272

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1				5					10					15	
Val Ala Ala Leu															
20															

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1					5					10				15

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
1 5 10 15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
1 5 10 15

Gly Gly Arg Arg Xaa Phe
20

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a
Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a
Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
1 5 10 15

Asn Val His Leu Val
20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCCG	60
TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG	120
GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCC	180
ATGATCCAC CGCTGGATTC CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC	240
GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG	300
CCGTGCCCCG TGTTGTGCCT GCCCCGTGC CAATCCCGGT CCCGATCATC ATTCCCCCGT	360
TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCCACCGC ACCGCCGACG ACGCCGGTGA	420
CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA	480
CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA	540
CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA	600
CCGTGCCCC GACCACGGTC GCTCCAGCCA CCGCCACGCC GACGACCGTC GCTCCGCAGC	660
CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AAGCCAGCAG CAGACCGTGG	720
CCCCGCAGAC GGTGGCGCCG GCTCCGCAGC CGCCGTCCGG TGGCCGCAAC GGCAGCGGCG	780
GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTCGCGGCT TCACTACGGT CGGAGGACAT	840
GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA	882

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

CCATCAACCA ACCGCTCGCG CCGCCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCGC      60
CGGTGCCTCC GGTGCCCCCG TTGCCCGCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC      120
CTAGGGCGCT GTTACGCCCC TGGTTGGCGG GGACGCCGCC GGCACCACCG GTACGCCCGA      180
TGGCGCCGTT GCCGCCGGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA      240
CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT      300
TCGTGCCCGT ACCGCCGGCA CCGCCGTTGC CGCCGTCACC GCCGACGAA CTACCGCGG      360
ACGCGGCCTG CCCGCCGGCG CCGCCCGCAC CGCCATTGGC ACCGCCGTCA CCGCCGGCTG      420
GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTCAACGAG      480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT      540
AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG      600
CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC      660
CCAGGCCAAT ACGGGGATAC CGGGTGTCTA AGCCGCCGCG AGCGCAGCTT CGGTTGCGCG      720
ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC      780
GGCGAGGGCA TCCACCACGC GTTGCGTCAG CTCGT                                815

```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTCACCGGG GCGGTTGAGC      60
CTTCTCCCAG AACAACTGCT GAAGATCCTC GCCCGCGAAA CAGGCGCTGA TTTGACGCTC      120
TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACCCTG GGGCTAACAG      180
GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCCGTGT CGCGGATCAG CTTTGCCGAC      240
GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GGCAGAGACC AGTATCCGAT CGAGACGCTG      300
GACGGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATCGT TGAGATGCTC      360
AAGCGTGAGC GCGACATCCA GCTCTTCACG ACCGACGGCC ACTACCAGGG CCGGATCTCA      420

```

ACACCCGACG TGTCATACGC GCCGCGGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT	480
GCGTTCTGCC TGTCGTTAAG CAAGCGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC	540
TTGATTGGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC	600
TCGCTGGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGAAAT	660
GCCGCAAAGG CATACTTCAC CGCGCTGGGG CATCTCGTCC CGCAGGAGTT CGCATTCCAG	720
GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGCCT CGGCTATTCTG	780
CTGCTGTACA AGAACATCAT AGGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT	840
TTCTACACC AGGATTCACG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC	900
GCTGAAACCG CTGGCCGGCT GCTCAGTGCC CGTACGTAAT CCGCTGCGCC CAGGCCGGCC	960
CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC	1020
ATACCGCCGG CAACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC	1080
GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTCG GCCCGACTTC CATTGCCTGC	1140
GTTCGGCACG AG	1152

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC	60
CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT	120
CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC	180
CGTGGTTTGC CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG	240
ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC	300
GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG	360
TGCAGCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC	420
TTGCCGACGG CGACCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG	480

TCCCGACGCT GGTGCGGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC 540
 TCACCGCCGC GGCACGTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC 600
 TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA 655

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
 1 5 10 15
 Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
 20 25 30
 Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
 35 40 45
 Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Pro Asp Asp Pro Thr Ala
 50 55 60
 Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
 65 70 75 80
 Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
 85 90 95
 Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
 100 105 110
 Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
 115 120 125
 Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
 130 135 140
 Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
 145 150 155 160
 Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
 165 170 175
 Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
 180 185 190
 Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro

195	200	205
Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro		
210	215	220
Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala		
225	230	235 240
Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn		
245	250	255
Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe		
260	265	

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro			
1	5	10	15
Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro			
20	25	30	
Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu			
35	40	45	
Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro			
50	55	60	
Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr			
65	70	75	80
Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro			
85	90	95	
Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser			
100	105	110	
Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro			
115	120	125	
Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile			
130	135	140	
Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala			
145	150	155	160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
 165 170

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr
100

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTT TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTGCGCG GACTGTGCGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	

CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652
Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala	
155 160 165	
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	
170 175 180	
CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG	748
His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu	
185 190 195	
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC	796
Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr	
200 205 210 215	
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC	844
Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn	
220 225 230	
GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT	892
Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr	
235 240 245	
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG	940
Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu	
250 255 260	
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA	988
Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln	
265 270 275	
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC	1036
Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn	
280 285 290 295	
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC	1084
Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile	
300 305 310	
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC	1132
Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala	
315 320 325	
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC	1180
Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly	

330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA			1333
GCGTGTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG			1393
GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG			1453
AGGCGATGGG TCGGATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC			1513
CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA			1573
CTACGGGGCG TTCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT			1633
CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT			1693
GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG			1753
TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC			1813
TCACAACGCT CCCGATGTGC CGGTGCTGAA CTAATTGCGC GCGACCCGG GCAACGGGGA			1873
GGGCATGTTG GTGTCCGGTC TGGTGTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC			1933
CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC			1993

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Val	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro
1				5					10					15	
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser
			20					25					30		
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
			35				40					45			
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu

50	55	60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr 65 70 75 80		
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala 85 90 95		
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly 100 105 110		
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser 115 120 125		
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys 130 135 140		
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr 145 150 155 160		
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro 165 170 175		
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr 180 185 190		
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly 195 200 205		
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly 210 215 220		
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu 225 230 235 240		
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala 245 250 255		
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn 260 265 270		
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe 275 280 285		
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro 290 295 300		
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn 305 310 315 320		
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu 325 330 335		
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val 340 345 350		

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365

Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCCGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAAATT CGTTTGCATA CGCTGTTGGC	180
CGTGTTGACC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCACCGAG	240
CGGTTTCGCCT GAAACGGGCG CCGGCGCCGG TACTGTCCGC ACTACCCCG CGTCGTCGCC	300
GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC	360
GGCCTTTCAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
CGGGATCGCG CAGGCCGCCG CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA	540
GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAAGTCCT	600
GGCGGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA	660
CCCCGGCGTG AACCTGCCCC GCACCGCGGT AGTTCCGCTG CACCGCTCCG ACGGGTCCGG	720
TGACACCTTC TTGTTACCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
GCCCCGGCTTC GGCACCACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG	840
CAACGGCGGC ATGGTGACCG GTTGCGCCGA GACACCGGGC TCGGTGGCCT ATATCGGCAT	900
CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCAACTAG GCAATAGCTC	960
TGGCAATTTT TTGTTGCCCG ACGCGCAAAG CATTGAGGCC GCGGCGGCTG GCTTCGCATC	1020
GAAAACCCCG GCGAACCAGG CGATTTTCGAT GATCGACGGG CCCGCCCGG ACGGCTACCC	1080
GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCCG CCACCGCGCA	1140

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GACCTTGCAG GCATTCTGTC ACTGGGCGAT CACCGACGGC AACAGGCCT CGTTCCTCGA      1200
CCAGGTTTCAT TTCCAGCCGC TGCCGCCCGC GGTGGTGAAG TTGTCTGACG CGTTGATCGC      1260
GACGATTTCCT AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG      1320
GCTGCTTTGTC GGAGCATGCT GGGCCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC      1380
CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG      1440
GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTTCATTT CTTCACCGCC      1500
ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC      1560
CGGTCGGCGC CTACTACGGG GCGTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA      1620
TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC      1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA      1740
GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG      1800
CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC      1860
CGGGCAACGG GGAGGGCATG TTGGTGCCG GTCTGGTGTT GGCGGTGATG GTCGTTCCCA      1920
TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG      1980
CGATCGGGAA TTC                                                                1993

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(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1           5           10           15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20           25           30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35           40           45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50           55           60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65           70           75           80

```

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser

370

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCCGA TTGAAGTCCA GGTACTCGTG	60
GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT	120
GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTT AGCGCTGATT TGCACAACAC	180
CTCGTGGAAG GTGATGCCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCCGATCCG	240
CTGCAACCCG GCAGCGCCCG TCGTCAACGG GCATCCCGTT CACCGCGACG GCTTGCCGGG	300
CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG	360
AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCCCGCACA GACAGGAGCC AGGCCTTATG	420
ACAGCATTCT GCGTCGAGCC CTACGGGCAG CCGAAGTACC TAGAAATCGC CGGGAAGCGC	480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCCACG	540
TCGTCTTACT TGTGGCGCAA CATCATGCCG CACTTGGAAG GGCTGGGCCG GCTGGTGGCC	600
TGCGATCTGA TCGGGATGGG CGCTTCGGAC AAGCTCAGCC CATCGGGACC CGACCGCTAT	660
AGCTATGGCG AGCAACGAGA CTTTTGTGTC GCGCTCTGGG ATGCGCTCGA CCTCGGCGAC	720
CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGGCGCTCG GCTTCGACTG GGCTAACCAG	780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG	840
GCGGACTGGC CGCCGGCCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGCGAG	900
CCAATGGCGT TGGAGCACAA CATCTTTGTC GAACGGGTGC TGCCCGGGGC GATCCTGCGA	960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CGGCGGCCAT TCGTGAACGG CGGCGAGGAC	1020
CGTCGCCCCA CGTTGTCGTG GCCACGAAAC CTTCCAATCG ACGGTGAGCC CGCCGAGGTC	1080
GTGCGGTTGG TCAACGAGTA CCGGAGCTGG CTCGAGGAAA CCGACATGCC GAAACTGTTC	1140
ATCAACGCCG AGCCCGGCGC GATCATCACC GGCCGCATCC GTGACTATGT CAGGAGCTGG	1200
CCCAACCAGA CCGAAATCAC AGTGCCCGGC GTGCATTTCT TTCAGGAGGA CAGCGATGGC	1260
GTCGTATCGT GGGCGGGCGC TCGGCAGCAT CGGCGACCTG GGAGCGCTCT CATTTACGGA	1320

GACCAAGAAT GTGATTTCGG GCGAAGGCGG CGCCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GCTCCGGGCA GAGATTCTCA GGGAAAAGGG CACCAATCGC AGCCGCTTCC TTCGCAACGA	1440
GGTCGACAAA TATACGTGGC AGGACAAAGG TCTTCCTATT TGCCAGCGA ATTAGTCGCT	1500
GCCTTTCTAT GGGCTCAGTT CGAGGAAGCC GAGCGGATCA CGCGTATCCG ATTGGACCTA	1560
TGGAACCGGT ATCATGAAAG CTTCGAATCA TTGGAACAGC GGGGGCTCCT GCGCCGTCGG	1620
ATCATCCAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTTACT AGCGCCAGC	1680
GCCGATCGGG AGGAGGTGCT GCGCGTCTG ACGAGCGAAG GTATAGGCGC GGTCTTTCAT	1740
TACGTGCCGC TTCACGATTC GCGGGCCGGG CGTCGCT	1777

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCCGTCCCG TGAATGCCCA TATCACGCAC	60
GGCCATGTTT TGGCTGTGCA CCTTCGCCCC ATGCCCGGAC GTTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CCGGGGGACG GTTGCGGGAA GGCGGCCAGG ATGTGCGTGA GCCGCGGCGC	180
CGCCGTGCGC CAGGCGACCG CTGGATGCTC AGCCCCGGTG CGGCGACGTA GCCAGCGTTT	240
GGCGCGTGTC GTCCACAGTG GTACTCCGGT GACGACGCGG CGCGGTGCCT GGGTGAAGAC	300
CGTGACCGAC GCCGCCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GCGGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG	60
AACGATTGAC GAACCGCTCG TCGGCGGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCACCC GGCCACTACG CGTCGAAGAC GTCCTCGCCG CCCGCAGCGA	180

GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCCGT CCTGTCGCTA TGGCTGCCTG	240
GGAAGCTCGC GTTCGGAAGC GATTTGCGTT CCTCACTGAC CTCGACGCCG ACGAGCAGCG	300
GTGGGCCGCC TGCAGCAAC GGCACCGCCG CGAAGTGGAG AACGCGCTGG CGGTGCTGCG	360
GTCCTGATCA ACCTGCCGGC GATCGTGCCG TTCCGCTGGC ACGGTTGCGG CTGGACGCGG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCCGGC TGTGGTGGTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCC TGATTCAGCA GGACCAATGG	540
AACTGCCCCG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT	600
GGCGTCATTC GGACATCGGT CCGGCTCGCG GGATCGTGGT GACGCCAGCG CTGAAGGAGT	660
GGAGCGCGGC GGTGCACGCG CTGCTGGACG GCCGGCAGAC GGTGCTGCTG CGTAAGGGCG	720
GGATCGGCGA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTTGTTGTTC CCGACGGTCG	780
CGCACAGCCA CGCCGAGCGG GTTCGCCCCG AGCACC CGA CCTGCTGGGC CCGCGGCCCG	840
CCGACAGCAC CGACGAGTGT GTGCTACTGC GGGCCG CAGC GAAAGTTGTT GCCGCACTGC	900
CGGTTAACCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCCGAGT	960
CGGTGCGCGC CGACCGGCTC GACTTTCGGC CCAAGCACAA ACTGGCCGTC TTGGTGGTCT	1020
CGGCGATCCC GCTGGCCGAG CCGGTCCGGC TGGCGCGTAG GCCCGAGTAC GGCGGTTGCA	1080
CCAGCTGGGT GCAGCTGCCG GTGACGCCGA CGTTGGCGGC GCCGGTGAC GACGAGGCCG	1140
CGCTGGCCGA GGTGCGCGCC CGGGTCCGCG AGGCCGTGGG TTGACTGGGC GGCATCGCTT	1200
GGTCTGAGC TGTACGCCA GTCGGCGCTG CGAGTGATCT GCTGTGGTT CGGTCCCTGC	1260
TGGCGTCAAT TGACGGCGCG GGCAACAGCA GCATTGGCGG CGCCATCCTC CGCGCGGCCG	1320
GCGCCACCG CTACAACC	1338

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CCGGCGGCAC CGGCGGCACC GGCGGTACCG GCGGCAACGG CGCTGACGCC GCTGCTGTGG	60
TGGGCTTCGG CGCGAACGGC GACCCTGGCT TCGCTGGCGG CAAAGGCGGT AACGGCGGAA	120
TAGGTGGGGC CGCGGTGACA GGCGGGGTCS CCGCGACGCG CGGCACCGGC GGCAAGGTG	180

GCACCGGCGG TGCCGGCGGC GCCGGCAACG ACGCCGGCAG CACCGGCAAT CCCGGCGGTA 240
 AGGGCGGCGA CGGCGGGATC GGCGGTGCCG GCGGGGCCGG CGGCGCGGCC GGCACCGGCA 300
 ACGGCGGCCA TGCCGGCAAC C 321

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAAGACCCGG CCCC GCCATA TCGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGACGCG 60
 GCGGCGTCGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CCGCACCGGA TGGCTGCTGC 120
 CGTTCGCCTC CGAACTCGTC ACTTCGGCGC AAGCCCGACG GCACCGCCGA ATCACCAGGG 180
 CGGTCCACGA TTCGGGTGCA AAGATCCTGC TGCAAATCCT GCACGCCGGA CGCTACGCCT 240
 ACCACCCACT TGCGGTCAGC GCCTCGCCGA TCAAGGCGCC GATCACCCCG TTTCGTCCGC 300
 GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGCGGA TTTCGCCCCG TGCGCGCAGT 360
 TGGCCCGCGA TGCCGGCTAC GACGGCGTCG AAATCATGGG CAGCGAAGGG TATCTGCTCA 420
 ATCAGTTCCT GGCGCCGCGC ACCAACAAGC GCACCGACTC GTGGGGCGGC ACACCGGCCA 480
 ACCGTGCGCG GT 492

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
 1 5 10 15
 Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
 20 25 30
 Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
 35 40 45
 His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro

50	55	60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu		
65	70	75 80
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys		
	85	90 95
Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys		
	100	105 110
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu		
	115	120 125
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala		
	130	135 140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly		
	145	150 155 160
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu		
	165	170 175
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp		
	180	185 190
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg		
	195	200 205
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp		
	210	215 220
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser		
	225	230 235 240
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg		
	245	250 255
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn		
	260	265 270
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr		
	275	280 285
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val		
	290	295 300
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met		
	305	310 315 320
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg		
	325	330 335
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val		
	340	345 350

Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp
 355 360 365
 Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg
 370 375 380
 Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Gln Leu
 385 390 395 400
 Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln
 405 410 415
 Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly
 420 425 430
 Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445
 Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460
 Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480
 Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510
 Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525
 His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15
 Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30
 Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110
 Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125
 Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg
 210 215 220
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTGCGC GATTGCGCCG CTACTCCTCC	60
GCCATGCACG CGATCGCCGG TTTCTCCGAT GCGTTGCGCC AAGAGCTGCG GGGTAGCGGA	120
ATCGCCGTCT CGGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTCGAC	180
CCCGCCGACA TGCCGCCGCC GTTTCGCAGC CTCACGCCCA TTCCCGTTCA CTGGGTGCGG	240
GCAGCGGTGC TTGACGGTGT GCGC	264

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TAGTCGGCGA CGATGACGTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG CGCGACCACG	60
AAGCCGGTGC GATCCTTACC CGCGAAGCAG TGGGTGAGCA CCGGGCGTCC GGCGGCAAGC	120
AGTGTGACGA CACGATGTAG CGCGCGCTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC	180
TCGTCGGTCA TGTAGCGGGT GGCCGCGTCA TTTATCGACT GGCTGGATTC GCCGGACTCG	240
CCGTTGGACC CGTCATTGGT TAGCAGCCTC TTGAATGCGG TTTCGTGCGG CGCTGAGTCG	300
TCGGCGTCAT CATCGGCGAG GTCGGGGAAC GGCAGCAGGT GGACGTCGAT GCCGTCCGGA	360
ACCCGTCCTG GACCGCGGCG GGCAACCTCC CGGGACGACC GCAGGTCGGC AACGTCGGTG	420
ATCCCCAGCC GGCAGCGCTG TGCCCTCGT GCCGAATTCG GCACGAGGCT GGCGAGCCAC	480
CGGGCATCAC CAAGCAACGC TTGCCAGTA CGGATCGTCA CTTCCGCATC CGGCAGACCA	540
ATCTCTCTGC CGCCCATCGT CAGATCCCGC TCGTGCGTTG ACAAGAACGG CCGCAGATGT	600
GCCAGCGGGT ATCGGAGATT GAACCGCGCA CGCAGTTCTT CAATCGCTGC GCGCTGCCGC	660
ACTATTGGCA CTTTCCGGCG GTCGCGGTAT TCAGCAAGCA TGCGAGTCTC GACGAACTCG	720
CCCCACGTAA CCCACGGCGT AGCTCCCGGC GTGACGCGGA GGATCGGCGG GTGATCTTTG	780
CCGCCACGCT CGTAGCCGTT GATCCACCGC TTCGCGGTGC CGGCGGGGAG GCCGATCAGC	840
TTATCGACCT CGGCGTATGC CGACGGCAAG CTGGGCGCGT TCGTCGAGGT CAAGAACTCC	900
ACCATCGGCA CCGGCACCAA GGTGCCGCAC CTGACCTACG TCGGCGACGC CGACATCGGC	960
GAGTACAGCA ACATCGGCGC CTCCAGCGTG TTCGTCAACT ACGACGGTAC GTCCAAACGG	1020

CGCACCACCG TCGGTTTCGA CGTACGGACC GGGTCCGACA CCATGTTTCGT GGCCCCAGTA 1080
 ACCATCGGCG ACGGCGCGTA TACCGGGGCC GGCACAGTGG TGCGGGAGGA TGTCCCGCCG 1140
 GGGGCGCTGG CAGTGTCGGC GGGTCCGCAA C 1171

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GCAAAGGCGG CACGGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG 60
 ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT 120
 TCACCCAAGG CGCCGACGGC AACGCCGCA ACGGCGGTGA CGGCGGGGTC GCGGGCAACG 180
 GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCC 227

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CCTCGCCACC ATGGGCGGGC AGGGCGGTAG CGGTGGCGCC GGCTCTACCC CAGGCGCCAA 60
 GGGCGCCAC GGCTTCACTC CAACCAGCGG CGGCGACGGC GGCACGGCG GCAACGGCGG 120
 CAACTCCCAA GTGGTCGGCG GCAACGGCGG CGACGGCGGC AATGGCGGCA ACGGCGGCAG 180
 CGCCGGCACG GCGGCAACG GCGGCCGGG CGGCGACGGC GCGTTTGGTG GCATGAGTGC 240
 CAACGCCACC AACCCTGGTG AAAACGGGCC AAACGGTAAC CCCGGCGGCA ACGGTGGCGC 300
 CGGC 304

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACAACATCGA CCAGCGCCGG CTCGGTGAGC	60
TGATCGACCT ATTTAACAGT GCGCGCTTCA GCCGGCAGGG CGAGCACCGC GCCCGGGATC	120
TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTTCG TCGCGCGGAA GGGAAAGCGG	180
GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCGT	240
CGAGTGGGCG GGTGTATGAC CCGTGCTGCG GTTCCGAGG CATGTTTGTG CAGACCGAGA	300
AGTTCATCTA CGAACACGAC GCGGATCCGA AGGATGTCTC GATCTATGGC CAGGAAAGCA	360
TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG	420
GGCTCGGCGC CCGATGGAGT GATACCTTCG CCCGCGACCA GCACCCGGAC GTGCAGATGG	480
ACTACGTGAT GGCCAATCCG CCGTTCAACA TCAAAGACTG GGCCCGCAAC GAGGAAGACC	540
CACGCTGGCG CTTCGGTGTT CCGCCCGCCA ATAACGCCAA CTACGCATGG ATTCAGCACA	600
TCCTGTACAA CTTGGCGCCG GGAGGTCGGG CGGGCGTGGT GATGGCCAAC GGGTCGATGT	660
CGTCGAACTC CAACGGCAAG GGGGATATTC GCGCGCAAAT CGTGGAGGCG GATTTGGTTT	720
CCTGCATGGT CGCSTTACCC ACCCAGCTGT TCCGCAGCAC CGGAATCCCG GTGTGCCTGT	780
GGTTTTTCGC CAAAAACAAG GCGGCAGGTA AGCAAGGGTC TATCAACCGG TCGGGCAGG	840
TGCTGTTTCAT CGACGCTCGT GAACTGGGCG ACCTAGTGGA CCGGGCCGAG CGGGCGCTGA	900
CCAACGAGGA GATCGTCCGC ATCGGGGATA CCTTCCACGC GAGCACGACC ACCGGCAACG	960
CCGGCTCCGG TGGTGCCGGC GGTAAATGGGG GCACTGGCCT CAACGGCGCG GCGGGTGCTG	1020
GCGGGGCGCG CGGCAACGCG GGTGTGCGCG GCGTGTCTT CCGCAACGCT GTGGGCGGCG	1080
ACGGCGGCAA CGGCGGCAAC GCGGGCCACG GCGGCGACGG CACGACGGGC GCGGCCGGCG	1140
GCAAGGGCGG CAACGGCAGC AGCGGTGCGG CCAGCGGCTC AGGCGTCGTC AACGTCACCG	1200
CCGGCCACGG CGGCAACGGC GGCAATGGCG GCAACGGCGG CAACGGCTCC GCGGGCGCCG	1260
GCGGCCAGGG CGGTGCCGGC GGCAGCGCCG GCAACGGCGG CCACGGCGGC GGTGCCACCG	1320
GCGGCGCCAG CGGCAAGGGC GGCAACGGCA CCAGCGGTGC CGCCAGCGGC TCAGGCGTCA	1380
TCAACGTCAC CGCCGGCCAC GCGGCAACG GCGGCAATGG CCGCAACGGC GGCAACGGC	1439

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GGGCCGGCGG GGCCGATTT TCTCGTGCCT TGATTGTGCG TGGGGATAAC GGCGGTGATG	60
GTGGTAACGG CGGGATGGGC GGGGCTGGCG GGGCTGGCGG CCCC GGCGGG GCCGGCGGCC	120
TGATCAGCCT GCTGGGCGGC CAAGGCGCCG GCGGGGCGCG CGGGACCGGC GGGGCCGGCG	180
GTGTTGGCGG TGACGGCGGG GCCGGCGGCC CCGGCAACCA GGCCTTCAAC GCAGGTGCCG	240
GCGGGGCGCG CGGCCTGATC AGCCTGCTGG GCGGCCAAGG CGCCGGCGGG GCCGGCGGGA	300
CCGGCGGGGC CGGCGGTGTT GGCGGTGAC	329

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GGCCGGAGGT AACTGTGGTG	60
CCGCCGGGCT GATCGGCAAC	80

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGGCTGTGTC GCACTCACAC CGCCGCATTC GGCGACGTTG GCCGCCCAAT ATCCAGCTCA	60
AGGCCTACTA CTTACCGTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA	120
TCAAGGTCAT CGACCGCGAC GGGCATCGAG GCCGTCGTCG CGCGGCTCGG GCAGGATCCG	180
CCCCGGCGCA CTTGCGCGCG CAAGCGGGCT CATCGCTCCG AACGGCGGCG ATCCTGTGAG	240
CACAAGTGAT GGCGCGCAAC GAGATTCGTC CAATTGTCAA GCCGTGTTCC ACCGCAGGGA	300
CCGGTTATAC GTATGTCAAC CTATGTCACT CGCAAGAACC GGCATAACGA TCCCGTGATC	360
CGCCGACAGC CCACGAGTGC AAGACCGTTA CA	392

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACCGGCGCCA CCGGCGGCAC CGGGTTCGCC GGTGGCGCCG GCGGGGCCGG CGGGCAGGGC	60
GGTATCAGCG GTGCCGGCGG CACCAACGGC TCTGGTGGCG CTGGCGGCAC CGGCGGACAA	120
GGCGGCGCCG GGGGCGCTGG CGGGGCCGGC GCCGATAACC CCACCGGCAT CGGCGGCGCC	180
GGCGGCACCG GCGGCACCGG CGGAGCGGCC GGAGCCGGCG GGGCCGGTGG CGCCATCGGT	240
ACCGGCGGCA CCGGCGGCGC GGTGGGCAGC GTCGGTAACG CCGGGATCGG CGGTACCGGC	300
GGTACGGGTG GTGTCTGGTG TGCTGGTGGT GCAGGTGCGG CTGCGGCCGC TGGCAGCAGC	360
GCTACCGGTG GCGCCGGGTT CGCCGCGGCG GCCGCGGAG AAGGCGGACC GGGCGGCAAC	420
AGCGGTGTGG GCGGCACCAA CGGCTCCGGC GGCGCCGGCG GTGCAGGCGG CAAGGGCGGC	480
ACCGGAGGTG CCGGCGGGTC CGGCGCGGAC AACCCACCG GTGCTGGTTT CGCCG	535

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CCGACGTGCG CGGGGCGATA CGGGGGTCAC CGACTACTAC ATCATCCGCA CCGAGAATCG	60
GCCGCTGCTG CAACCGCTGC GGGCGGTGCC GGTTCATCGGA GATCCGCTGG CCGACCTGAT	120
CCAGCCGAAC CTGAAGGTGA TCGTCAACCT GGGCTACGGC GACCCGAACCT ACGGCTACTC	180
GACGAGCTAC GCCGATGTGC GAACGCCGTT CGGGCTGTGG CCGAACGTGC CGCCTCAGGT	240
CATCGCCGAT GCCCTGGCCG CCGGAACACA AGAAGGCATC CTTGACTTCA CGGCCGACCT	300
GCAGGCGCTG TCCGCGCAAC CGCTCACGCT CCCGAGATC CAGCTGCCGC AACCCGCCGA	360
TCTGGTGGCC GCGGTGGCCG CCGCACCGAC GCCGCGGAG GTGGTGAACA CGCTCGCCAG	420
GATCATCTCA ACCAACTACG CCGTCCTGCT GCCCACCCTG GACATCGCCC TCGCCTGGTC	480
ACCACCCTGC CGCTGTACAC CACCCAACTG TTCGTCAGGC AACTCGCTGC GGGCAATCTG	540

ATCAACGCGA TCGGCTATCC CCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG 600
 CGGCGTGGAA TTGCTCACCC TCCTCGCGGC GGCCTCGGAC ACCGTTGAA ACATCGAGGG 660
 CCTCGTCACC TAACGGATTG CCGACGGCAT 690

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACGGTGACGG CGGTACTGGC GGCGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT 60
 TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG 120
 GCTCTGGGGG CACCGGCGGC GACGGCGGGA CCGGCGGGCG TGGCGGCCTG TTAATGGGCG 180
 CCGGCGCCGG CGGGCACGGT GGCACCTGGC GCGCGGGCGG TGCCGGTGTC GACGGTGGCG 240
 GCGCCGGCGG GGCCGGCGGG GCCGGCGGCA ACGGCGGCGC CGGGGGTCAA GCCGCCCTGC 300
 TGTTGGGGCG CGGCGGCACC GCGGAGCCG GCGGCTACGG CGGCGATGGC GGTGGCGGCG 360
 GTGACGGCTT CGACGGCACG ATGGCCGGCC TGGGTGGTAC CGGTGGC 407

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GATCGGTCAG CGCATCGCCC TCGGCGGCAA GCGATTCCGC GGTCTCACCG AAGAACATCG 60
 TGCACGCGGC GCGCGGACC AGCCCGCTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC 120
 ACAGCCAGTC CTTGGCGGCC TCGAGGCGA ACACGTCCGT GTCACCGGTG TAGATCGCCG 180
 GGATGCCCCG CTCCGCCAAC GCATTCCGGC ACGCCCGCGC GTCTTTGTGA TGCTCGACGA 240
 TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGCGGAA GGTGGCCCCG CTGGCCAGTA 300
 GCGCCGCGAC GTCGGCGGCC AGGTCGTCCG GGATGTGCCG GCGCAGCGCT CCGGCGCGAC 360
 GCGCGAAAAA CGACCCCTCA CCCAGCTGGG TCCCGCTGGC ATATCCCTTG CCGTCCTGGG 420
 CGATATTGGA CGCGCATGCC CCGACCGCT ACAGGCCGCG CACCACCG 468

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```
GGTGGTAACG GCGGCCAGGG TGGCATCGGC GCGCCCGCG AGAGAGGCGC CGACGGCGCC      60
GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CGGTGGCGAC      120
GGCGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCCCG GTACACCGAC      180
GGCGCCACGG GCACCGGCGG CGACGGCGGC AACGGCGGC      219
```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```
TAGTCCGGC GAGGGCGGCA AGGGCGGCGA CGGTGGCCAC GGCGGTGACG GCGTCGGCGG      60
CAACAGTTCC GTCACCCAAG GCGGCAGCGG CGGTGGCGGC GGCGCCGGCG GCGCCGGCGG      120
CAGCGGCTTT TTCGGCGGCA AGGGCGGCTT CGGCGGCGAC GGCGGTCAGG GCGGCCCCAA      180
CGGCGGCGGT ACCGTCGGCA CCGTGGCCGG TGGCGGCGGC AACGGCGGTG TCGGCGGCCG      240
GGGCGGCGAC GGCGTCTTTG CCGGTGCCGG CGGCCAGGGC GGCCTCGGTG GGCAGGGCGG      300
CAATGGCGGC GGCTCCACCG GCGGCAACGG CGGCCTTGCG GCGCGGGCGG GTGGCGGAGG      360
CAACGCCCCG GCTCGTGCCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTCGCTGC      420
CATCGCATCA GGCGCGTACT GCCCCGAACA CCTGGAACAT CACCCGAGTT AGCGGGGCGC      480
ATTTCCTGAT CACC                                         494
```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGGAGG CGCGGCGGGT GCCGTTGGGG	60
TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCCC	120
CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GCGTCGGCG	180
GCCAGAGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC	220

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ATGGCGGCAA CGGGGGCCCC GCGGTGCTG GCGGGGCCGG CGACTACAAT TTCCAACGGC	60
GGGCAGGGTG GTGCCGGCGG CCAAGGCGGC CAAGGCGGCC TGGGCGGGGC AAGCACCACC	120
TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG	180
CCGCGTTGGA CCAGGCCGGC ATCACCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA	240
AGGCGATGTG TGGGCTGTGT GCTAACGGCG TAACAGGTCT ACAGCTGGTC GCGGACCTGC	300
GGGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG	360
GCGCGTACTG CCCCGAACAC CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCAAG	60
ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT	120
TCACCCAAAG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCCGGC ACCACAGGCG	240
GCGACGGCGG GGCCGGCGGG GCCGGCGGAA CCGGCGGAAC CGGCGGAGCC GCCGGCACCG	300
GCACCGGCGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CGGCGGCAAA GGCGGCACCG	360

GCGGCGACGG TGCACTCTCA GGCAGCACCG GTGGTGCCGG

400

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGCAACGGCG GCAACGGCGG CATGCCCGG ATTGGGCGG AACGGCGTTC CGGGACGGGC	60
AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGGCGG	120
CAACAGCGGC ACCGGCAGCG GCGACGGCGG TGCCGGCGGG AACGGCGGCG CGGCGGGCAC	180
GGGCGGCACC GCGGCGGACG GCGGCCTCAC CGGTACTGGC GGCACCGGCG GCAGCGGTGG	240
CACCGGCGGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC	300
GCAGGCGGGC GGTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGCG GGGCCGGGGC	360
CGGCGGCGGT GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCCGGCGG	420
CGATGGCGGC AACGGGGCCA TCGGCGGCCA CGGCCCACTC ACTGACGACC CCGGCGGCAA	480
CGGGGGCACC GCGGCAACG GCGGCACCGG CGGCACCGGC GCGCGGGCA TCGGCAGC	538

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GGGCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG	60
TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCCG AGCGGCCGGC GCCGACGCCC	120
CGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCGTCGGCG	180
GCCACGGCGG CAACGCCATT GCCGCGGCA TCAACGGCTC CGGTGGTGCC GGCGGCACC	239

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGCAGCGCTA CCGGTGGCGC CGGGTTCGCC GCGGCGCCCG GCGGAGAAGG CGGAGCGGGC	60
GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGGCGGCG CCGGCGGTGC AGGCGGCAAG	120
GGCGGCACCG GAGGTGCCGG CGGGTCCGGC GCGGACAACC CCACCGGTGC TGGTTTCGCC	180
GGTGGCGCCG GCGGCACAGG TGGCGCGGCC GCGCCCGCGG GGGCCGCGCG GCGGACCGGT	240
ACCGGCGGCA CCGGCGGCGT TGTCGGCGCC ACCGGTAGTG CAGGCATCGG CGGGGCGGCG	300
GGCGCGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCCT CTCCGGCTTT	360
GACGGCGGCC AAGGCGGCCA AGGCGGGGCC GCGGCGAGCG CCGGCGCCCG CGGCATCAAC	420
GGGGCCGGCG GGGCCGGCGG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCCGCA	480
GGTCTCGGCG ACAACGGCGG GGTCCGCGGT GACGGTGGGG CCGGTGGCGC CGCCGGCAAC	540
GGCGGCAACG CCGGCGTCGG CCTGACAGCC AAGGCCGGCG ACGGCGGCGC CGCGGGCAAT	600
GGCGGCAACG GGGGCGCCGG CGGTGCTGGC GGGGCGGCG ACAACAATTT CAACGGCGGC	660
CAGGGTGGTG CCGGCGGCCA AGGCGGCCAA GCGGCTTGG GCGGGCAAG CACCACCTGA	720
TCGGCCTAGC CGCACCCGGG AAAGCCGATC CAACAGGCGA CGATGCCGCC TTCCTTGCCG	780
CSTTGGACCA GGCCGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCCAAGG	840
CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGGTCGCG GACCTGCGGG	900
AATACAATCC CGGGCTGACC ATGGACAGCG CGGCCAAGTT CGCTGCCATC GCATCAGGCG	960
CGTACTGCCC CGAACACCTG GAACA	985

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTTCG CGATGCCGGC	120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG	240

AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCATGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGCGGCTA AAAACGCCGC CCAACAGCTG GTATTGTCCG	360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT	540
CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTTTG	660
CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCGA CGTCAAGCGG TTCCGGGGGT	720
TTGACAACTG GGAAGGCGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAACGGC	780
AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTCTG	840
CGCAGCTGCA CGTGTGGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG	900
AACGGCTTTA CGCGGAAAC CCTTCGGCCC GCGACCAAAT TCTCCCGGTG TACGCGGAGT	960
ATCAGCAGAG GTCGGAGAAG GTGCTGACCG AATAACAAC CAAGGCAGCC CTGGAACCGG	1020
TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCCGCCT CCGCAAGAGC	1080
AGGGATTGAT CCCTGGCTTC CTGATGCCGC CGTCTGACGG CTCCGGTGTG ACTCCCGSTA	1140
CCGGGATGCC AGCCGCACCG ATGGTTCCGC CTACCGGATC GCCGGGTGGT GGCCTCCCGG	1200
CTGACACGGC GGCGCAGCTG ACGTCGGCTG GCGGGGAAGC CGCAGCGCTG TCGGGCGACG	1260
TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCGG CGGGGTGCCG TCGGCGCCGT	1320
TGGGATCCGC GATCGGGGGC GCCGAATCGG TGCGGCCCGC TGGCGCTGGT GACATTGCCG	1380
GCTTAGGCCA GGAAGGGCC GCGGCGGGC CCGCGCTGGG CGGCGGTGGC ATGGGAATGC	1440
CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG	1500
ACGAGGCGCT CTACACCGAG GATCGGGCAT GGACCGAGGC CGTCATTGGT AACCGTCGGC	1560
GCCAGGACAG TAAGGAGTCG AAGTGAGCAT GGACGAATTG GACCCGCATG TCGCCCGGGC	1620
GTTGACGCTG GCGGCGCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA	1680
CGGATCCTTC CCGCCACCG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA	1740
GTGGCTCACC GGCCTGCGCA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGCGGT	1800
GGCTCAGCGG GTCAACGAGG CGCTGCACAA TGCGCAGGCC GCGGCGTCCG CGTATAACGA	1860

CGCGGCGGGC GAGCAGCTGA CCGCTGCGTT ATCGGCCATG TCCCGCGCGA TGAACGAAGG 1920
 AATGGCCTAA GCCCATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCCGCAATGC 1980
 GGTCAATCAG CGCGCCCGAC ACGGCGTGAG TACGCATTGT CAATGTTTTG ACATGGATCG 2040
 GCCGGGTTTCG GAGGGCGCCA TAGTCCTGGT CGCCAATATT GCCGCAGCTA GCTGGTCTTA 2100
 GGTTCGGTTA CGCTGGTTAA TTATGACGTC CGTTACCA 2138

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1 5 10 15
 Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20 25 30
 Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
 35 40 45
 Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50 55 60
 Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
 65 70 75 80
 Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85 90 95
 Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
 100 105 110
 Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
 115 120 125
 Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
 130 135 140
 Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
 145 150 155 160
 Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
 165 170 175
 Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
 180 185 190

Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln
 195 200 205
 Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro
 210 215 220
 Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro
 225 230 235 240
 Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg
 245 250 255
 Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro
 260 265 270
 Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Gly Val
 355 360 365
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Ala	Gly	Asn	Val	Thr	Ser	Ala	Ser	Gly	Pro	His	Arg	Phe	Gly	Ala	Pro	1	5	10	15
Asp	Arg	Gly	Ser	Gln	Arg	Arg	Arg	Arg	His	Pro	Ala	Ala	Ser	Thr	Ala	20	25	30	
Thr	Glu	Arg	Cys	Arg	Phe	Asp	Arg	His	Val	Ala	Arg	Gln	Arg	Cys	Gly	35	40	45	
Phe	Pro	Pro	Ser	Arg	Arg	Gln	Leu	Arg	Arg	Arg	Val	Ser	Arg	Glu	Ala	50	55	60	
Thr	Thr	Arg	Arg	Ser	Gly	Arg	Arg	Asn	His	Arg	Cys	Gly	Trp	His	Pro	65	70	75	80
Gly	Thr	Gly	Ser	His	Thr	Gly	Ala	Val	Arg	Arg	Arg	His	Gln	Glu	Ala	85	90	95	
Arg	Asp	Gln	Ser	Leu	Leu	Leu	Arg	Arg	Arg	Gly	Arg	Val	Asp	Leu	Asp	100	105	110	
Gly	Gly	Gly	Arg	Leu	Arg	Arg	Val	Tyr	Arg	Phe	Gln	Gly	Cys	Leu	Val	115	120	125	
Val	Val	Phe	Gly	Gln	His	Leu	Leu	Arg	Pro	Leu	Leu	Ile	Leu	Arg	Val	130	135	140	
His	Arg	Glu	Asn	Leu	Val	Ala	Gly	Arg	Arg	Val	Phe	Arg	Val	Lys	Pro	145	150	155	160
Phe	Glu	Pro	Asp	Tyr	Val	Phe	Ile	Ser	Arg	Met	Phe	Pro	Pro	Ser	Pro	165	170	175	
His	Val	Gln	Leu	Arg	Asp	Ile	Leu	Ser	Leu	Leu	Gly	His	Arg	Ser	Ala	180	185	190	
Gln	Phe	Gly	His	Val	Glu	Tyr	Pro	Leu	Pro	Leu	Leu	Ile	Glu	Arg	Ser	195	200	205	
Leu	Ala	Ser	Gly	Ser	Arg	Ile	Ala	Phe	Pro	Val	Val	Lys	Pro	Pro	Glu	210	215	220	
Pro	Leu	Asp	Val	Ala	Leu	Gln	Arg	Gln	Val	Glu	Ser	Val	Pro	Pro	Ile	225	230	235	240
Arg	Lys	Val	Arg	Glu	Arg	Cys	Ala	Leu	Val	Ala	Arg	Phe	Glu	Leu	Pro	245	250	255	

Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His
 260 265 270

Pro Arg Arg Ile Gly
 275

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15

Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30

Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45

Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60

Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80

Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95

Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110

Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125

Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140

Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160

Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175

His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro
 35 40 45
 Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val
 50 55 60
 Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala
 65 70 75 80
 Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln
 85 90 95
 Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His
 100 105 110
 Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val
 115 120 125
 Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val
 130 135 140
 Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His
 145 150 155 160
 His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly
 165 170 175
 Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val
 180 185 190
 Gly Gly Ser Ala
 195

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Val	Arg	Cys	Gly	Thr	Leu	Val	Pro	Val	Pro	Met	Val	Glu	Phe	Leu	Thr	1	5	10	15
Ser	Thr	Asn	Ala	Pro	Ser	Leu	Pro	Ser	Ala	Tyr	Ala	Glu	Val	Asp	Lys	20	25	30	
Leu	Ile	Gly	Leu	Pro	Ala	Gly	Thr	Ala	Lys	Arg	Trp	Ile	Asn	Gly	Tyr	35	40	45	
Glu	Arg	Gly	Gly	Lys	Asp	His	Pro	Pro	Ile	Leu	Arg	Val	Thr	Pro	Gly	50	55	60	
Ala	Thr	Pro	Trp	Val	Thr	Trp	Gly	Glu	Phe	Val	Glu	Thr	Arg	Met	Leu	65	70	75	80
Ala	Glu	Tyr	Arg	Asp	Arg	Arg	Lys	Val	Pro	Ile	Val	Arg	Gln	Arg	Ala	85	90	95	
Ala	Ile	Glu	Glu	Leu	Arg	Ala	Arg	Phe	Asn	Leu	Arg	Tyr	Pro	Leu	Ala	100	105	110	
His	Leu	Arg	Pro	Phe	Leu	Ser	Thr	His	Glu	Arg	Asp	Leu	Thr	Met	Gly	115	120	125	
Gly	Glu	Glu	Ile	Gly	Leu	Pro	Asp	Ala	Glu	Val	Thr	Ile	Arg	Thr	Gly	130	135	140	
Gln	Ala	Leu	Leu	Gly	Asp	Ala	Arg	Trp	Leu	Ala	Ser	Leu	Val	Pro	Asn	145	150	155	160
Ser	Ala	Arg	Gly	Ala	Thr	Leu	Arg	Arg	Leu	Gly	Ile	Thr	Asp	Val	Ala	165	170	175	
Asp	Leu	Arg	Ser	Ser	Arg	Glu	Val	Ala	Arg	Arg	Gly	Pro	Gly	Arg	Val	180	185	190	
Pro	Asp	Gly	Ile	Asp	Val	His	Leu	Leu	Pro	Phe	Pro	Asp	Leu	Ala	Asp	195	200	205	
Asp	Asp	Ala	Asp	Asp	Ser	Ala	Pro	His	Glu	Thr	Ala	Phe	Lys	Arg	Leu	210	215	220	
Leu	Thr	Asn	Asp	Gly	Ser	Asn	Gly	Glu	Ser	Gly	Glu	Ser	Ser	Gln	Ser	225	230	235	240
Ile	Asn	Asp	Ala	Ala	Thr	Arg	Tyr	Met	Thr	Asp	Glu	Tyr	Arg	Gln	Phe	245	250	255	
Pro	Thr	Arg	Asn	Gly	Ala	Gln	Arg	Ala	Leu	His	Arg	Val	Val	Thr	Leu	260	265	270	
Leu	Ala	Ala	Gly	Arg	Pro	Val	Leu	Thr	His	Cys	Phe	Ala	Gly	Lys	Asp	275	280	285	

Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp
 290 295 300

Arg Asp Val Ile Val Ala Asp
 305 310

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTCGTGCCGA TTCGGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTCGCCGA CGGGCTGGCC GGCAAGGGTA AGCAAATCAA CACCACGCTG AACAGCCTGT	120
CGCAGGCGTT GAACGCCTTG AATGAGGGCC GCGGCGACTT CTTGCGGGTG GTACGCAGCC	180
TGGCGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTCGCG TTGAACAAGA	240
ACCTTGCGGA GTTCACCGAC AGGTTGACCC ACTCCGATGC GGACCTGTG AACGCCATCC	300
AGCAATTCGA CAGCTTGCTC GCCGTCGCGC GCCCGTTCTT CGCCAAGAAC CGCGAGGTGC	360
TGACGCATGA CGTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCAG CCCGATCCGT	420
TGGATGGGTT GGAGACCGTC CTGCACATCT TCCCGACGCT GGCGGGCAAC ATTAACCAGC	480
TTTACCATCC GACACACGGT GGCCTGGTGT CGCTTTCCGC GTTCACGAAT TTCGCCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTGAGG CGGGTAGCCG GCTCGGTTAT CAAGAGTCGG	600
CCGAACTCTG TGCGCAGTAT CTGGCGCCAG TCCTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTCGGCCT GAACGTGGCC AGCACCGCCT CGACACTGCC TAAAGAGATC GCGTACTCCG	720
AGCCCCGCTT GCAGCCGCCC AACGGGTACA AGGACACCAC GGTGCCCGGC ATCTGGGTGC	780
CGGATACGCC GTTGTCACAC CGCAACACGC AGCCCGGTTG GGTGGTGGCA CCCGGGATGC	840
AAGGGGTTCA GGTGGGACCG ATCACGCAGG GTTTGCTGAC GCCGGAGTCC CTGGCCGAAC	900
TCATGGGTGG TCCCGATATC GCCCCTCCGT CGTCAGGGCT GCAAACCCCG CCCGGACCCC	960
CGAATGCGTA CGACGAGTAC CCCGTGCTGC CGCCGATCGG TTTACAGGCC CCACAGGTGC	1020
CGATACCACC GCCGCCTCCT GGGCCCGACG TAATCCCGGG TCCGGTGCCA CCGGTCTTGG	1080
CGGCGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AAACCTTCGAC TACATGGGCC	1140

TCTTGTGCT	GTGCGCGGC	CTGGCGACCT	TCCTGTTCCG	GGTGTCTCT	AGCCCCGCCC	1200
GTGGAACGAT	GGCCGATCGG	CACGTGTTGA	TACCGGCGAT	CACCGGCCTG	GCGTTGATCG	1260
CGGCATTTCG	CGCACATTTC	TGGTACCGCA	CAGAACATCC	GCTCATAGAC	ATGCGCTTGT	1320
TCCAGAACCG	AGCGGTGCGG	CAGGCCAACA	TGACGATGAC	GGTGTCTCTC	CTCGGGCTGT	1380
TTGGCTCCTT	CTTGCTGCTC	CCGAGCTACC	TCCAGCAAGT	GTTGCACCAA	TCACCGATGC	1440
AATCGGGGGT	GCATATCATC	CCACAGGGCC	TCGGTGCCAT	GCTGGCGATG	CCGATCGCCG	1500
GAGCGATGAT	GGACCGACGG	GGACCGGCCA	AGATCGTGCT	GGTTGGGATC	ATGCTGATCG	1560
CTGCGGGGTT	GGGCACCTTC	GCCTTTGGTG	TCGCGCGGCA	AGCGGACTAC	TTACCCATTC	1620
TGCCGACCGG	GCTGGCAATC	ATGGGCATGG	GCATGGGCTG	CTCCATGATG	CCACTGTCCG	1680
GGGCGGCAGT	GCAGACCCTG	GCCCCACATC	AGATCGCTCG	CGGTTGACG	CTGATCAGCG	1740
TCAACCAGCA	GGTGGGCGGT	TCGATAGGGA	CCGCACTGAT	GTCGGTGCTG	CTCACCTACC	1800
AGTTCAATCA	CAGCGAAATC	ATCGCTACTG	CAAAGAAAGT	CGCACTGACC	CCAGAGAGTG	1860
GCGCCGGGCG	GGGGGCGGCG	GTTGACCCTT	CCTCGCTACC	GCGCCAAACC	AACTTCGCGG	1920
CCCAACTGCT	GCATGACCTT	TCGCACGCCT	ACGCGGTGGT	ATTCTGTGATA	GCGACCGCGC	1980
TAGTGGTCTC	GACGCTGATC	CCCGCGGCAT	TCCTGCCGAA	ACAGCAGGCT	AGTCATCGAA	2040
GAGCACCGTT	GCTATCCGCA	TGACGTCTGC	TT			2072

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCACCCCGGA	GAAGTCGTT	GTGACGACC	TGGACATCGA	CTCGCTGTCG	ATGGTCGAGA	60
TCGCCGTGCA	GACCGAGGAC	AAGTACGGCG	TCAAGATCCC	CGACGAGGAC	CTCGCCGGTC	120
TGCGTACCGT	CGGTGACGTT	GTCGCCTACA	TCCAGAAGCT	CGAGGAAGAA	AACCCGGAGG	180
CGGCTCAGGC	GTTGCGCGCG	AAGATTGAGT	CGGAGAACCC	CGATGCGGCA	CGAGCAGATC	240
GGTGCCTTTC	ACCCACATCG	CAAGCTCGAG	ACGCCGCTCG	TCCTCTTGCA	CGCTCAGCCA	300
GTTTGGCGTG	TCGCCGCCTT	CCAGCAAGTG	TTCCCACCAC	ACGAAGGGAC	CCTCGCGAAA	360
GGTGACTGAT	CCGCGGACCA	CATAGTCGAT	GCCACCGTGG	CTGACAATTG	CGCCGGGTCC	420

GAGTTGGCGG GGGCCGAATT GCGGCATTGC GTCGAAGGCC AGCGGATCCC GGCGCCCGCC	480
CGGCGTGGCT GGTGTTTTGG GCCGCCGAT GGCCACGACG AGAACGACGA TGGCGGCGAT	540
GAACAGCGCC ACGGCAATCA CGACCAGCAG ATTTCCACG CATACCCTCT CGTACCGCTG	600
CGCCGCGGTT GGTCGATCGG TCGCATATCG ATGGCGCCGT TTAACGTAAC AGCTTTCGCG	660
GGACCGGGGG TCACAACGGG CGAGTTGTCC GGCCGGGAAC CCGGCAGGTC TCGGCCGCGG	720
TCACCCACG TCACTGGTGC ACCATCCGGG TGTCGGTGAG CGTGCAACTC AAACACACTC	780
AACGGCAACG GTTTCTCAGG TCACCAGCTC AACCTCGACC CGCAATCGCT CGTACGTTTC	840
GACCGCGCGC AGGTCGCGAG TCAGCAGCTT TGCGCCGGCA GCTTTCGCCG TGAAGCCGAC	900
CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGGT CGGTCAAGCC	960
GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCCG CCAAGTAGGC	1020
GTGGACGGCA ACAGGGGCAA TACGATGCGG CGGTGGTAGC CGGGTCAAGA CCGAATAGGT	1080
TTCCACAGCC GCGTGCGCA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CGGCGGCCTC	1140
GTGCCCTTCG TGCCAGGTG CGAATCCGGC AACCAGCACG CTGGTGTCTG GTGCGATCAC	1200
CGCCGTGTGC GATCGAGCGT TTCCCGAACG ATTTGTCGG TCAACGGGGG CAGGGGACGT	1260
TCTGCCCCTG CGACGAGAAC CGAGCCTTC CGAACGAGTT CGACACCGGT CGGGGCCGGC	1320
TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTGTTCCC GCGCAAGCCA	1380
AGGCGCTCGC GAATCCGCTT GGGAATCACC AGACGTCCTG CGACATCGAT GGTGTTTCGC	1440
ATGGTAGGAA ATTTACCATC GCACGTTCCA TAGGCGTGTC CTGCGCGGGA TGTCGGGACG	1500
ATCCGCTAGC GTATCGAACG ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG	1560
ATGGGTGTG ATCCCGGGTT GACCCGATGC GGGCTGTGCG TCATCGAGAG TGGGCGTGGT	1620
CGGCAGCTCA CCGCGCTGGA TGTCGACGTG GTGCGCACAC CGTCGGATGC GGCCTTGCGG	1680
CAGCGCCTGT TGGCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG	1740
GTGGTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACC GCG	1800
CAGGCCGGCG GCGTGATCGC CCTGGCGGCG GCCAAACGTG GTGTCGACGT GCATTTCCAT	1860
ACCCCCAGCG AGGTCAAGGC GGCGGTCACT GGCAACGGTT CCGCAGACAA GGCTCAGGTC	1920
ACC	1923

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

CTGGCGTGCC AGTGTACCG GCGATATGAC GTCGGCATT C AATTTGCGG CCCCCCGGA      60
CCCGTCGCCA CCAATCTGG ACCACCCGGT CCGTCAATTG CCGAAGGTCG CCAAGTGCGT      120
GCCCCAATGTG GTGCTGGGTT TCTTGAACGA AGGCCTGCCG TATCGGGTGC CCTACCCCCA      180
AACCAACGCCA GTCCAGGAAT CCGGTCCCGC GCGGCCGATT CCCAGCGGCA TCTGCTAGCC      240
GGGGATGGTT CAGACGTAAC GGTGCTAGT GTCGAAACCC GCGCCAGGGC CGCTGGACGG      300
GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG      360
AGTGCTTGGT GGTTCGTGTT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA      420
GGGGACAACG TGCTTTTGCC TCTTGGTCCG CTTTGCCGC CCGACGCGGT GGTGGCGAAA      480
CGGGCTGAGT CGGGAATGCT CGGCGGGTTG TCGGTTCCGC TCAGCTGGGG AGTGGCTGTG      540
CCACCCGATG ATTATGACCA CTGGGCGCCT GCGCCGAGG ACGGCGCCGA TGTCGATGTC      600
CAGGCGGCCG AAGGGGCGGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG      660
GCGTGGAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGGAGTAGC      720
AGCAGCGTGA TTCCGCATTC TCCGGCGGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA      780
TTTGACCAAGT GATCGGCGGT CTCGGTGTTT CCGCGGCCGG CTATGACAAC AGTCAATGTG      840
CATGACAAGT TACAGGTATT AGGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC      900
GTTTTATGAC GGATCCGCAC GCGATGCGGG ACATGGCGGG CCGTTTTGAG GTGCACGCCC      960
AGACGGTGGA GGACGAGGCT CGCCGGATGT GGGCGTCCGC GCAAAACATC TCGGGNGCGG      1020
GCTGGAGTGG CATGGCCGAG GCGACCTCGC TAGAC                                1055

```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```

CCGCTCGTT GTTGGCATAC TCCGCGCGG CCGCTCGAC CGCACTGGCC GTGGCGTGTG      60

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TCCGGGCTGA CCACCGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG 120
 CGCAGCTGGT CACCCAGCCA CCGGGCGGTG TGCGACAGCG CCTGCATCAC CTTGGTATAG 180
 CCGTCGCGCC CCAGCCGCAG GAAGTTGTAG TACTGGCCCA CCACCTGGTT ACCGGGACGG 240
 GAGAAGTTCA GGGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACCAGA 300
 TCCTCCGGCA GGTGCTCGGG CCCGCGCCAC ACGACAAACC CGACGCCGGG ATAGGTCAG 359

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AACGGGCCCC TGGGCACCGC TCCTCTAAGG GCTCTCGTTG GTCGCATGAA GTGCTGGAAG 60
 GATGCATCTT GGCAGATTCC CGCCAGAGCA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC 120
 CGCAAAGTTC CTCGAATAAC TCCGTACCCG GAGCGCCAAA CCGGGTCTCC TTCGCTAAGC 180
 TGCGCGAACC ACTTGAGGTT CCGGGACTCC TTGACGTCCA GACCGATTCTG TTCGAGTGGC 240
 TGATCGGTTC GCCGCGCTGG CGCGAATCCG CCGCCGAGCG GGGTGATGTC AACCCAGTGG 300
 GTGGCCTGGA AGAGGTGCTC TACGAGCTGT CTCCGATCGA GGACTTCTCC 350

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp
 1 5 10 15
 Gly Leu Ala Gly Lys Gly Lys Gln Ile Asn Thr Thr Leu Asn Ser Leu
 20 25 30
 Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala
 35 40 45
 Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Gln Asp Asp
 50 55 60

Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg
 65 70 75 80
 Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp
 85 90 95
 Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val
 100 105 110
 Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Thr Leu Leu
 115 120 125
 Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro
 130 135 140
 Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 185 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315 320
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe

355	360	365
Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu		
370	375	380
Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His		
385	390	395 400
Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val		
405	410	415
Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu		
420	425	430
Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu		
435	440	445
Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln		
450	455	460
Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro		
465	470	475 480
Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met		
485	490	495
Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile		
500	505	510
Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp		
515	520	525
Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met		
530	535	540
Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala		
545	550	555 560
Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln		
565	570	575
Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr		
580	585	590
Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu		
595	600	605
Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser		
610	615	620
Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser		
625	630	635 640
His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser		
645	650	655

Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg
 660 665 670

Arg Ala Pro Leu Leu Ser Ala
 675

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
 1 5 10 15
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
 20 25 30
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
 35 40 45
 Tyr Ile Gln Lys Leu Glu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
 50 55 60
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
 65 70 75 80
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110
 Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser

20	25	30
Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu		
35	40	45
Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser		
50	55	60
Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala		
65	70	75 80
Gly Asp Gly Ser Asp Val Thr Val Gly		
85		

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ala Ser Thr Ala Leu Ala		
1	5	10 15
Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp		
20	25	30
His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly		
35	40	45
Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln		
50	55	60
Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly		
65	70	75 80
Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro		
85	90	95
Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys		
100	105	110
Pro Asp Ala Gly Ile Gly Gln		
115		

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
 1 5 10 15
 Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
 20 25 30
 Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
 35 40 45
 Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
 50 55 60
 Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
 65 70 75 80
 Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
 85 90 95
 Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
 100 105 110
 Glu Asp Phe Ser
 115

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGCTACGCAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCGTCGCTGC TGGCGATGGC 60
 GTGAAAGCCG CCGACGTGTT CGCCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG 120
 GTGCGGGCCG CCATCGATCG GGTGCGCCGAC GAGCGCACGT GCACGCACTG TCAACACCAC 180
 GCCGGTGTTC CGTTGCCGTT CGAGCTGCCA TGAGGGTGCT GCTGACCGGC GCGGCCGGCT 240
 TCATCGGGTC GCGCGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTCG 300
 ACGCGCTGCT GCCCGCCCG CACGGGCCAA ACCCGGTGCT GCCACCGGGC TGCCAGCGGG 360
 TCGACGTGCG CGACGCCAGC GCGCTGGCCC CGTTGTTGGC CGGTGTCGAT CTGGTGTGTC 420
 ACCAGGCCGC CATGGTGGGT GCCGGCGTCA ACGCCGCCGA CGCACC CGCC TATGGCGGCC 480
 ACAACGATTT CGCCACCACG GTGCTGCTGG CGCAGATGTT CGCCGCCGGG GTCCGCCGTT 540

TGGTGCTGGC GTCGTCGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCCCAGCATG	600
GACCGGTCGA CCCGCTGCCG CGGCGGCGAG CCGACCTGGA CAATGGGGTC TTCGAGCACC	660
GTTGCCCCGGG GTGCGGCGAG CCAATCATCT GGCAATTGGT CGACGAAGAT GCCCCGTTGC	720
GCCCCGCGCAG CCTGTACGCG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC	780
GGAAACGAAT GGCGGTTCGG TGGTGGCGTT G	811

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GTCCCCGCGAT GTGGCCGAGC ATGACTTTTCG GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTCGGC GTTGGTCAGC GTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAGT CGCGAGCGTA	180
ACGTCACGGT CAAATATCGC GTGGAATTTC GCCGTGACGT TCCGCTCGCG GACAATCAAG	240
GCATACTCAC TTACATGCCA GCCATTGGA CGGGTTCGAT CGCCTTCGGG CTGGTGAACG	300
TGCCGGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCACG	360
CCAAGGACAA CGGACGCATC CCGTACAAGC GCGTCTGCGA GCGGTGTGGC GAGGTGGTCG	420
ACTACCGCGA TCTTGCCCGG GCCTACGAGT CCGGCGACGG CCAAATGGTG GCGATCACCG	480
ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTCTG	540
TCCCCGCCGC CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTTC GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTGCTGCTGG CTAAGACACT CGCCGAGACC GACCGGATGG	660
CGATCGTGGA TCGCCCCACC GGCCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAGT	780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA	840
TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCCTGCC GCGCGACCTC	900
AAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCAGTTCC GGCGGGTCGG CTCATCGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CCGCACCGCC GGCAATACCG CCAGCGCCAC CGTTACCGCC GTTTGCGCCG TTGCCCCCGT	60
TGCCGCCCCGT CCCGCCGGCC CCGCCGATGG AGTTCTCATC GCCAAAAGTA CTGGCGTTGC	120
CACCGGAGCC GCCGTTGCCG CCGTCACCGC CAGCCCCGCC GACTCCACCG GCCCCACCGA	180
CTCCGCCGCT GCCACCGTTG CCGCCGTTGC CGATCAACAT GCCGCTGGCG CCACCCTTGC	240
CACCCACGCC ACCGGCTCCG CCCACCCCGC CGACACCAAG CGAGCTGCCG CCGGAGCCAC	300
CATCACCACC TACGCCACCG ACCGCCAGA CACCAGCGAC CGGGTCTTCG TGAAACGTCG	360
CGGTGCCACC ACCGCCGCCG TTACCGCCAA CCCCACCGGC AACGCCGGCG CCGCCATCCC	420
CGCCGGCCCC GCGTTGCCG CCGTTGCCGC CGTTGCCGAA CAACAACCCG CCGGCGCCGC	480
CGTTGCCGCC CGCGCCGCCG GTCCCGCCGG CGCCGCCGAC GCCAAGGCCG CTGCCGCCCT	540
TGCCGCCATC ACCACCCCTG CCGCCGACCA CATCGGGTTC TGCCTCGGGG TCTGGGCTGT	600
CAAACCTCGC GATGCCAGCG TTGCCGCCGC TTCCCCCGGG CCCCCCGTG GCGCCGTCAC	660
CACCGATACC ACCCGCGCCA CCGGCGCCAC CGTTGCCGCC ATCACCGAAT AGCAACCCGC	720
CGGCGCCACC ATTGCCGCCA GCTCCCCCTG CGCCACCGTC GCGCGCCGAG GCGGCACTGG	780
CAGCCCCGTT ACCACCGAAA CCGCCGCTAC CACCGGTAGA GGTGGCAGTG GCGATGTGTA	840
CGAAAGCGCC GCCTCCGGCG CCGCCGCTAC CACCCCCACT GCCGGCGGCT ACACCGTCGG	900
ACCCGTTGCC ACCATCACCG CCAAAGGCGC TCGCAATGTC GCCCTGCGCG ACTCCGCCGT	960
CGCCGCCGTT GCCCGCGCCG CCACCGGCAG CGGCGGTACC GCCGTCACCA CCGGCACCGC	1020
CGGTGGCCTT GCCCGAGCCT GCGGTCGCGG TGGCACCGTC GCCGCCGGTG CCACCGGTG	1080
GCCTGCCGGC AGTGCCATGG CCGCCCGTGC CGCCGTCGCC GCCGTTTGA TCACCGATGC	1140
CGGACACATC TGCCGGGCTG TCCCCGGTGC TGGCCGCGGG GCCGGGCGTG GGATTGACCC	1200
CGTTTGCCCC GCGGAGGCCG GCGCCGCCGG TACCACCGGC GCCGCCATGG CCGAACAGCC	1260
CGGCGTTGCC GCCGTTACCG CCGGCACCCC CGATGCCTGC GGCCACGCTG GTGCCGCCGA	1320
CACCGCCGTT GCCCGCGTTG CCCCACAACC ACCCCCCGTT CCCACCGGCA CCGCCGGCCG	1380


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CGCCGGTACC ACCGGCCCCG CCGTTGCCGC CGTTGCCGAT CAACCCGGCC GCGCCTCCGC      1440
TGCCGCCGGT TTGACCGAAC CCGCCAGCCG CGCCGTTGCC ACCGTTGCCA AACAGCAACC      1500
CGCCGGCCGC GCCAGGCTGC CCGGGTGCCG TCCCGTCGGC GCCGTTTCCG ATCAACGGGC      1560
GCCCCAAAAG CGCCTCGGTG GCGCATTCA CCGCACCAG CAGACTCCGC TCAACAGCGG      1620
CTTCAGTGCT GGCATACCGA CCCGCGGCCG CAGTCAACGC CTGCACAAAC TGCTCGTGAA      1680
ACGCTGCCAC CTGTACGCTG AGCGCCTGAT ACTGCCGAGC ATGGGCCCCG AACAAACCCG      1740
CAATCGCCGC CGACACTTCA TCGGCAGCCG CAGCCACCAC TTCCGTCGTC GGGATCGCCG      1800
CGGCCGCATT AGCCGCGCTC ACCTGCGAAC CAATAGTCGA TAAATCCAAA GCCGCAGTTG      1860
CCAGCAGCTG CGGCGTCGCG ATCACCAAGG ACACCTCGCA CCTCCGGATA CCCCATATCG      1920
CCGCACCGTG TCCCAGCGG CCACGTGACC TTTGGTCGCT GGCTGGCGGC CCTGACTATG      1980
GCCGCGACGG CCCTCGTTCT GATTGCCCCC GGCGCGCAGC TTGTTGCGCG AGTTGAAGAC      2040
GGGAGGACAG GCCGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGGCG      2100
AGATGAATAG GCGGACGCCG ATCTCCTTGT TGCTGAGTCC CTCACCGACC AGTAGAGCCA      2160
CCTCAAGCTC TGTCGGTGTC AACGCGCCCC AGCCACTTGT CGGGCGTTTC CGTGCACCGC      2220
GGCCTCGTTG CGCGTACGCG ATCGCCTCAT CGATCGATAA CGCAGTTCCT TCGGCCCAGG      2280
CATCGTCGAA CTCGCTGTCA CCCATGGATT TTCGAAGGGT GGCTAGCGAC GAGTTACAGC      2340
CCGCCTGGTA GATCCCSAAG CGGACCG                                     2367

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(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
1           5           10           15

Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
20           25           30

Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
35           40           45

Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
50           55           60

```

Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp
 65 70 75 80
 Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr
 85 90 95
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg
 100 105 110
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala
 115 120 125
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly
 130 135 140
 His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly
 145 150 155 160
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly
 165 170 175
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr
 180 185 190
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala
 195 200 205
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala
 210 215 220
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg
 225 230 235 240
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala
 245 250 255
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys
 260 265 270
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu
 275 280 285
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe
 290 295 300
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350

Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365

Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GGCCAAAACG CCCCGGCGAT CGCGGCCACC GAGGCCGCCT ACGACCAGAT GTGGGCCCCAG	60
GACGTGGCGG CGATGTTTGG CTACCATGCC GGGGCTTCGG CGGCCGTCTC GGCGTTGACA	120
CCGTTGCGCC AGGCGCTGCC GACCGTGGCG GGCGGCGGTG CGCTGGTCAG CGCGGCCGCG	180
GCTCAGGTGA CCACGCGGGT CTTCCGCAAC CTGGGCTTGG CGAACGTCCG CGAGGGCAAC	240
GTCCGCAACG GTAATGTCCG GAACTTCAAT CTCGGCTCGG CCAACATCGG CAACGGCAAC	300
ATCGGCAGCG GCAACATCGG CAGCTCCAAC ATCGGGTTTG GCAACGTGGG TCCTGGGTTG	360
ACCGCAGCGC TGAACAACAT CGGTTTCGGC AACACCGGCA GCAACAACAT CGGGTTTGGC	420
AACACCGGCA GCAACAACAT CGGGTTCGGC AATACCGGAG ACGGCAACCG AGGTATCGGG	480
CTCAGGGTA GCGGTTTGTT GGGGTTTCGGC GGCCTGAACT CGGGCACCGG CAACATCGGT	540
CTGTTCAACT CGGGCACCGG AAACGTCGGC ATCGGCAACT CGGGTACCGG GAACTGGGGC	600
ATTGGCAACT CGGGCAACAG CTACAACACC GGTTTTGGCA ACTCCGGCGA CGCCAACACG	660
GGCTTCTTCA ACTCCGGAAT AGCCAACACC GGCGTCGGCA ACGCCGGCAA CTACAACACC	720
GGTAGCTACA ACCCGGGCAA CAGCAATACC GGCGGCTTCA ACATGGGCCA GTACAACACG	780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGCTTGCAA ACTCCGGCAA TGTCAACACC	840
GGCGCCTTCA TTA CTGGCAA CTTCAACAAC GGCTTCTTGT GGCGCGGCGA CCACCAAGGC	900
CTGATTTTCG GGAGCCCCGG CTTCTTCAAC TCGACCAGTG CGCCGTCGTC GGGATTCTTC	960
AACAGCGGTG CCGGTAGCGC GTCCGGCTTC CTGAACTCCG GTGCAACAA TTCTGGCTTC	1020
TTCAACTCTT CGTCGGGGGC CATCGGTAAC TCCGGCCTGG CAAACGCGGG CGTGCTGGTA	1080
TCGGGCGTGA TCAACTCGGG CAACACCGTA TCGGGTTTGT TCAACATGAG CCTGGTGGCC	1140
ATCACAACGC CGGCCTTGAT CTCGGGCTTC TTCAACACCG GAAGCAACAT GTCGGGATTT	1200

TTCGGTGGCC CACCGGTCTT CAATCTCGGC CTGGCAAACC GGGGCGTCGT GAACATTCTC	1260
GGCAACGCCA ACATCGGCAA TTACAACATT CTCGGCAGCG GAAACGTCGG TGAATTCAAC	1320
ATCCTTGGCA GCGGCAACCT CGGCAGCCAA AACATCTTGG GCAGCGGCAA CGTCGGCAGC	1380
TTCAATATCG GCAGTGAAAA CATCGGAGTA TTCAATGTCT GTTCCGGAAG CCTGGGAAAC	1440
TACAACATCG GATCCGGAAA CCTCGGGATC TACAACATCG GTTTTGGAAA CGTCGGCGAC	1500
TACAACGTCG GCTTCGGGAA CGCGGGCGAC TTCAACCAAG GCTTTGCCAA CACCGGCAAC	1560
AACAACATCG GGTTCGCCAA CACCGGCAAC AACAACATCG GCATCGGGCT GTCCGGCGAC	1620
AACCAGCAGG GCTTCAATAT TGCTAGCGGC TGGAACCTCG GCACCGGCAA CAGCGGCCTG	1680
TTCAATTCGG GCACCAATAA CGTTGGCATC TTCAACGCGG GCACCGGAAA CGTCGGCATC	1740
GCAAACCTCG GCACCGGGAA CTGGGGTATC GGAACCCCG GTACCGACAA TACCGGCATC	1800
CTCAATGCTG GCAGCTACAA CACGGGCATC CTCAACGCCG GCGACTTCAA CACGGGCTTC	1860
TACAACACGG GCAGCTACAA CACCGGCGGC TTCAACGTCG GTAACACCAA CACCGGCAAC	1920
TTCAACGTGG GTGACACCAA TACCGGCAGC TATAACCCCG GTGACACCAA CACCGGCTTC	1980
TTCAATCCCG GCAACGTCAA TACCGGCCTT TCGACACGG GCGACTTCAA CAATGGCTTC	2040
TTGGTGGCGG GCGATAACCA GGGCCAGATT GCCATCGATC TCTCGGTAC CACTCCATTC	2100
ATCCCCATAA ACGAGCAGAT GGTCAATTGAC GTACACAACG TAATGACCTT CGGCGGCAAC	2160
ATGATCACGG TCACCGAGGC CTCGACCGTT TTCCCCAAA CCTTCTATCT GAGCGGTTTG	2220
TTCTTCTTCG GCCCGGTCAA TCTCAGCGCA TCCACGCTGA CCGTTCCGAC GATCACCTTC	2280
ACCATCGGCG GACCGACGGT GACCGTCCCC ATCAGCATTG TCGGTGCTCT GGAGAGCCGC	2340
ACGATTACCT TCCTCAAGAT CGATCCGGCG CCGGGCATCG GAAATTCGAC CACCAACCCC	2400
TCGTCCGGCT TCTTCAACTC GGGCACCGGT GGCACATCTG GCTTCCAAA CGTCGGCGGC	2460
GGCAGTTCAG GCGTCTGGAA CAGTGGTTTG AGCAGCGCGA TAGGGAATTC GGGTTTCCAG	2520
AACCTCGGCT CGCTGCAGTC AGGCTGGGCG AACCTGGGCA ACTCCGTATC GGGCTTTTTTC	2580
AACACCAGTA CCGTGAACCT CTCCACGCCG GCCAATGTCT CGGGCCTGAA CAACATCGGC	2640
ACCAACCTGT CCGCGTGTGTT CCGCGGTCCG ACCGGGACGA TTTTCAACGC GGGCCTTGCC	2700
AACCTGGGCC AGTTGAACAT CGGCAGCGCC TCGTGCCGAA TTCGGCACGA GTTAGATACG	2760
GTTTCAACAA TCATATCCGC GTTTTGCGGC AGTGCATCAG ACGAATCGAA CCCGGGAAGC	2820

GTAAGCGAAT AAACCGAATG GCGGCCTGTC AT

2852

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln
 1 5 10 15
 Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr
 50 55 60
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr

225		230		235		240
Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly						
	245			250		255
Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu						
	260		265			270
Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe						
	275		280			285
Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly						
	290		295		300	
Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe						
305		310		315		320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn						
	325		330			335
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile Gly Asn Ser Gly						
	340		345			350
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn						
	355		360			365
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro						
370		375		380		
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe						
385		390		395		400
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val						
	405		410			415
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly						
	420		425			430
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly						
	435		440			445
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly						
450		455		460		
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn						
465		470		475		480
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly						
	485		490			495
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn						
	500		505			510
Gln Gly Phe Ala Asn Thr Gly Asn Asn Ile Gly Phe Ala Asn Thr						
	515		520			525

Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly
 530 535 540

Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu
 545 550 555 560

Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly
 565 570 575

Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn
 580 585 590

Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr
 595 600 605

Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620

Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640

Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655

Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670

Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685

Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700

Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720

Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735

Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750

Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765

Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780

Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800

Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815

Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
820 825 830

Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
835 840 845

Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
850 855 860

Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
865 870 875 880

Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
885 890 895

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
930 935 940

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTGCGA

38

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCGCATGCGA GCCACGTGCC CACAACGGCC

30

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTTCATGGAA TTCTCAGGCC GGTAAGGTCC GCTGCGG 37

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG 60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CTTTCGCTT TCTTCCCTTC 120
CTTTCTCGCC ACGTTCGCCG GCTTTCCCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG 180
GTTCCGATTT AGTGCTTTAC GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC 240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT 300
CTTTAATAGT GGACTCTTGT TCCAACTGG AACAACTC AACCTATCT CCGTCTATTC 360
TTTTGATTTA TAAGGGATTT TGCCGATTC GGCCTATTGG TTAAAAAATG AGCTGATTTA 420
ACAAAAATTT AACGCGAATT TTAACAAAT ATTAACGTTT ACAATTTTCA GTGGCACTTT 480
TCGGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA 540
TCCGCTCATG AATTAATTCT TAGAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT 600
TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCCG TTTCTGTAAT GAAGGAGAAA 660
ACTCACCGAG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCTGCG ATTCCGACTC 720
GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA 780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC 840
AGACTTGTTT AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC 900
CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAAGGAC 960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT 1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGAATGC TGTTTTCCCG GGGATCGCAG 1080

TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATTCCGT CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC	1200
CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT CGATAGATTG	1260
TCGCACCTGA TTGCCCCGACA TTATCGCGAG CCCATTTATA CCCATATAAA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA	1440
CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA	1500
GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG	1560
GTGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC	1620
AGAGCGCAGA TACCAAATAC TGTCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG	1680
AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCACT GGCTGCTGCC	1740
AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG	1800
CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC	1860
ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA	1920
AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT	1980
CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG	2040
CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG	2100
GCCTTTTAC GGTTCTGGC CTTTGTCTGG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA	2160
TCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC	2220
AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG CCTGATGCGG	2280
TATTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA	2340
CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGTATACACT CCGCTATCGC TACGTGACTG	2400
GGTCATGGCT GCGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGCT	2460
GCTCCCGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC GGGAGCTGCA TGTGTCAGAG	2520
GTTCACCG TCATACCGA AACGCGCGAG GCAGCTGCGG TAAAGCTCAT CAGCGTGGTC	2580
GTGAAGCGAT TCACAGATGT CTGCCTGTTT ATCCGCGTCC AGCTCGTTGA GTTTCTCCAG	2640
AAGCGTTAAT GTCTGGCTTC TGATAAAGCG GGCCATGTTA AGGGCGGTTT TTTCCTGTTT	2700

GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTTCATG GGGGTAATGA TACCGATGAA	2760
ACGAGAGAGG ATGCTCACGA TACGGGTTAC TGATGATGAA CATGCCCGGT TACTGGAACG	2820
TTGTGAGGGT AAACAACTGG CGGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG	2880
TCAATGCCAG CGCTTCGTTA ATACAGATGT AGGTGTTCCA CAGGGTAGCC AGCAGCATCC	2940
TGCGATGCAG ATCCGGAACA TAATGGTGCA GGGCGCTGAC TTCCGCGTTT CCAGACTTTA	3000
CGAAACACGG AAACCGAAGA CCATTCATGT TGTGCTCAG GTCGCAGACG TTTTGACGCA	3060
GCAGTCGCTT CACGTTTCGCT CGCGTATCGG TGATTCAATC TGCTAACCAG TAAGGCAACC	3120
CCGCCAGCCT AGCCGGGTCC TCAACGACAG GAGCACGATC ATGCGCACCC GTGGGGCCGC	3180
CATGCCGGCG ATAATGGCCT GCTTCTCGCC GAAACGTTTG GTGGCGGGAC CAGTGACGAA	3240
GGCTTGAGCG AGGGCGTGCA AGATTCGAA TACCGCAAGC GACAGGCCGA TCATCGTCGC	3300
GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT GACCCAGAGC GCTGCCGGCA CCTGTCCTAC	3360
GAGTTGCATG ATAAAGAAGA CAGTCATAAG TGCGGCGACG ATAGTCATGC CCCGCGCCCA	3420
CCGGAAGGAG CTGACTGGGT TGAAGGCTCT CAAGGGCATC GGTGAGATC CCGGTGCCTA	3480
ATGAGTGAGC TAACTTACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA	3540
CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT	3600
TGGGCGCCAG GGTGGTTTTT CTTTTCACCA GTGAGACGGG CAACAGCTGA TTGCCCTTCA	3660
CCGCCTGGCC CTGAGAGAGT TGCAGCAAGC GGTCCACGCT GGTTTGCCCC AGCAGGCGAA	3720
AATCCTGTTT GATGGTGGTT AACGGCGGGA TATAACATGA GCTGTCTTCG GTATCGTCGT	3780
ATCCCACTAC CGAGATATCC GCACCAACGC GCAGCCCGGA CTCGGTAATG GCGCGCATTG	3840
CGCCCAGCGC CATCTGATCG TTGGCAACCA GCATCGCAGT GGGAACGATG CCCTCATTTA	3900
GCATTTGCAT GGTGTGTTGA AAACCGGACA TGGCACTCCA GTCGCCTTCC CGTTCCGCTA	3960
TCGGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC AGCCAGACGC AGACGCGCCG	4020
AGACAGAACT TAATGGGCCC GCTAACAGCG CGATTTGCTG GTGACCCAAT GCGACCAGAT	4080
GCTCCACGCC CAGTCGCGTA CCGTCTTCAT GGGAGAAAAT AATACTGTTG ATGGGTGTCT	4140
GGTCAGAGAC ATCAAGAAAT AACGCCGGAA CATTAGTGCA GGCAGCTTCC ACAGCAATGG	4200
CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCCCACT GACGCGTTGC GCGAGAAGAT	4260
TGTGCACCGC CGCTTTACAG GCTTCGACGC CGCTTCGTTT TACCATCGAC ACCACCACGC	4320
TGGCAGCCAG TTGATCGGCG CGAGATTTAA TCGCCGCGAC AATTTGCGAC GGCGCGTGCA	4380

GGGCCAGACT	GGAGGTGGCA	ACGCCAATCA	GCAACGACTG	TTTGCCCGCC	AGTTGTTGTG	4440
CCACGCGGTT	GGGAATGTAA	TTCAGCTCCG	CCATCGCCGC	TTCCACTTTT	TCCCGCGTTT	4500
TCGCAGAAAC	GTGGCTGGCC	TGGTTCACCA	CGCGGGAAAC	GGTCTGATAA	GAGACACCGG	4560
CATACTCTGC	GACATCGTAT	AACGTTACTG	GTTTCACATT	CACCACCCTG	AATTGACTCT	4620
CTTCCGGGCG	CTATCATGCC	ATACCGCGAA	AGGTTTTGCG	CCATTTCGATG	GTGTCCGGGA	4680
TCTCGACGCT	CTCCCTTATG	CGACTCCTGC	ATTAGGAAGC	AGCCCAGTAG	TAGGTTGAGG	4740
CCGTTGAGCA	CCGCCGCCGC	AAGGAATGGT	GCATGCAAGG	AGATGGCGCC	CAACAGTCCC	4800
CCGGCCACGG	GGCCTGCCAC	CATACCCACG	CCGAAACAAG	CGCTCATGAG	CCCGAAGTGG	4860
CGAGCCCGAT	CTTCCCCATC	GGTGATGTCT	GCGATATAGG	CGCCAGCAAC	CGCACCTGTG	4920
GCGCCGCTGA	TGCCGGCCAC	GATGCGTCCG	GCGTAGAGGA	TCGAGATCTC	GATCCCGCGA	4980
AATTAATACG	ACTCACTATA	GGGGAATTGT	GAGCGGATAA	CAATTCCCCT	CTAGAAATAA	5040
TTTTGTTTAA	CTTTAAGAAG	GAGATATACA	TATGGGCCAT	CATCATCATC	ATCACGTGAT	5100
CGACATCATC	GGGACCAGCC	CCACATCCTG	GGAACAGGCG	GCGGCGGAGG	CGGTCCAGCG	5160
GGCGCGGGAT	AGCGTCGATG	ACATCCGCGT	CGCTCGGGTC	ATTGAGCAGG	ACATGGCCGT	5220
GGACAGCGCC	GGCAAGATCA	CCTACCGCAT	CAAGCTCGAA	GTGTCGTTCA	AGATGAGGCC	5280
GGCGCAACCG	AGGGGCTCGA	AACCACCGAG	CGGTTGCGCT	GAAACGGGCG	CCGGCGCCGG	5340
TACTGTGCGG	ACTACCCCGG	CGTCGTGCGC	GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	5400
GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	GGCCTTTCAC	GAGAGGTATC	CGAACGTCAC	5460
GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	CGGGATCGCG	CAGGCCGCCG	CCGGGACGGT	5520
CAACATTGGG	GCCTCCGACG	CCTATCTGTC	GGAAGGTGAT	ATGGCCGCGC	ACAAGGGGCT	5580
GATGAACATC	GCGCTAGCCA	TCTCCGCTCA	GCAGGTCAAC	TACAACCTGC	CCGGAGTGAG	5640
CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	GGCGGCCATG	TACCAGGGCA	CCATCAAAAC	5700
CTGGGACGAC	CCGCAGATCG	CTGCGCTCAA	CCCCGGCGTG	AACCTGCCCG	GCACCGCGGT	5760
AGTTCCGCTG	CACCGCTCCG	ACGGGTCCGG	TGACACCTTC	TTGTTACCCC	AGTACCTGTC	5820
CAAGCAAGAT	CCCAGGGGCT	GGGGCAAGTC	GCCCCGCTTC	GGCACCACCG	TCGACTTCCC	5880
GGCGGTGCCG	GGTGCGCTGG	GTGAGAACGG	CAACGGCGGC	ATGGTGACCG	GTTGCGCCGA	5940
GACACCGGGC	TGCGTGGCCT	ATATCGGCAT	CAGCTTCCTC	GACCAGGCCA	GTCAACGGGG	6000

ACTCGGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTTT TTGTTGCCCC ACGCGCAAAG	6060
CATTCAGGCC GCGGCGGCTG GCTTCGCATC GAAAACCCCG GCGAACCAGG CGATTTCGAT	6120
GATCGACGGG CCCGCCCCCG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA	6180
CAACCGGCAA AAGGACGCCG CCACCGCGCA GACCTTGCAG GCATTTCTGC ACTGGGCGAT	6240
CACCGACGGC AACAAGGCCT CGTTCCTCGA CCAGGTTTAT TTCCAGCCGC TGCCGCCCGC	6300
GGTGGTGAAG TTGTCTGACG CGTTGATCGC GACGATTTCC AGCGCTGAGA TGAAGACCGA	6360
TGCCGCTACC CTCGCGCAGG AGGCAGGTAA TTTGAGCGG ATCTCCGGCG ACCTGAAAAC	6420
CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCGTTGCAG GGCCAGTGGC GCGGCGCGGC	6480
GGGGACGGCC GCCCAGGCCG CGGTGGTGCG CTTCCAAGAA GCAGCCAATA AGCAGAAGCA	6540
GGAACCTCGAC GAGATCTCGA CGAATATTCG TCAGGCCGGC GTCCAATACT CGAGGGCCGA	6600
CGAGGAGCAG CAGCAGGCGC TGTCTCGCA AATGGGCTTT GTGCCACAA CGGCCGCTC	6660
GCCGCCGTCG ACCGCTGCAG CGCCACCCGC ACCGGCGACA CCTGTTGCCC CCCCACCACC	6720
GGCCGCCGCC AACACGCCGA ATGCCAGCC GGGCGATCCC AACGCAGCAC CTCCGCCGGC	6780
CGACCCGAAC GCACCGCCGC CACCTGTCAT TGCCCCAAAC GCACCCCAAC CTGTCCGGAT	6840
CGACAACCCG GTTGGAGGAT TCAGCTTCGC GCTGCCTGCT GGCTGGGTGG AGTCTGACGC	6900
CGCCCACTTC GACTACGGTT CAGCACTCCT CAGCAAAACC ACCGGGGACC CGCCATTTCC	6960
CGGACAGCCG CCGCCGGTGG CCAATGACAC CCGTATCGTG CTCGGCCGGC TAGACCAAAA	7020
GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTTGG GCTCGGACAT	7080
GGGTGAGTTC TATATGCCCT ACCCGGGCAC CCGGATCAAC CAGGAAACCG TCTCGCTTGA	7140
CGCCAACGGG GTGTCTGGAA GCGCGTCGTA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA	7200
GCCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCCC GCGGCGAACG CACCGGACGC	7260
CGGGCCCCCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCCAACAACC CGGTGGACAA	7320
GGGCGCGGCC AAGGCGCTGG CCGAATCGAT CCGGCCTTTG GTCGCCCCGC CGCCGGCGCC	7380
GGCACCGGCT CCTGCAGAGC CCGCTCCGGC GCCGGCGCCG GCCGGGAAG TCGCTCCTAC	7440
CCCACGACA CCGACACCGC AGCGGACCTT ACCGGCCTGA GAATTCTGCA GATATCCATC	7500
AACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC	7560
CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCTTGG	7620
GGCCTCTAAA CGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACATAT CCGGAT	7676

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

Met Gly His His His His His His Val Ile Asp Ile Ile Gly Thr Ser
1           5           10           15

Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
20           25           30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
35           40           45

Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
50           55           60

Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
65           70           75           80

Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
85           90           95

Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
100          105          110

Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
115          120          125

Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
130          135          140

Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145          150          155          160

Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
165          170          175

Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
180          185          190

Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
195          200          205

Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
210          215          220

Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
225          230          235          240

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Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
 245 250 255
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
 260 265 270
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
 275 280 285
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp
 290 295 300
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
 305 310 315 320
 Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525

Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540

Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560

Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575

Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590

Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620

Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640

Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655

Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670

Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685

Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700

Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720

Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735

Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750

Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765

Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780

Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800

Pro Ala

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GTGGCGGCGC	TGCGGCCGGC	CAGCAGAGCG	ATGTGCATCC	GTTTCGGAAC	CTGATCGCGG	60
TCGACGATGA	GCGCGCCGAA	CGCCGCGACG	ACGAAGAACG	TCAGGAAGCC	GTCCAGCAGC	120
GCGGTCCGCG	CGGTGACGAA	GCTGACCCCG	TCGCAGATCA	GCAGCACCCC	GGCGATGGCG	180
CCGACCAATG	TCGACCGGCT	GATCCGCCGC	ACGATCCGCA	CCACCAGCGC	CACCAGGACC	240
ACACCCAGCA	GGGCGCCGGT	GAACCGCCAG	CCGAATCCGT	TGTGACCGAA	GATGGCCTCC	300
CCGATCGCGA	TCAGCTGCTT	ACCGACCGGC	GGGTGAACCA	CCAGGCCGTA	CCCGGGGTTG	360
TCTTCCACCC	CATGGTTGTT	CAGCACCTGC	CAGGCCTGGC	GGTGCGTAAT	GCTTCTCGTC	420
GAAGATGGGG	GTGCCGGCAT	CCGTCACCGA	GCCC			454

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TGCAGAAGTA	CGGCGGATCC	TCGGTGGCCG	ACGCCGAACG	GATTGCGCCG	GTGCGCGAAC	60
GCATCGTCGC	CACCAAGAAG	CAAGGCAATG	ACGTCGTCGT	CGTCGTCTCT	GCCATGGGGG	120
ATACCACCGA	CGACCTGCTG	GATCTGGCTC	AGCAGGTGTG	CCCGGCGCCG	CCGCCTCGGG	180
AGCTGGACAT	GCTGCTTACC	GCCGGTGAAC	GCATCTCGAA	TGCGTTGGTG	GCCATGGCCA	240
TCGAGTCGCT	CGGCGCGCAT	GCCCGGTCGT	TCACCGGTTT	GCAGGCCGGG	GTGATCACCA	300
CCGGCACCCA	CGGCAACGCC	AAGATCATCG	ACGTCACGCC	GGGGCGGCTG	CAAACCGCCC	360
TTGAGGAAGG	GCGGGTCGTC	TTGGTGGCCG	GATTCCAAGG	GGTCAGCCAG	GACACCAAGG	420
ATGTCACGAC	GTTGGGCCGC	GGCGGCTCGG	ACACCACCGC	CGTCGCCATG		470

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GGCCGGCGTA	CCCGGCCGGG	ACAAACAACG	ATCGATTGAT	ATCGATGAGA	GACGGAGGAA	60
TCGTGGCCCT	TCCCCAGTTG	ACCGACGAGC	AGCGCGCGGC	CGCGTTGGAG	AAGGCTGCTG	120
CCGCACGTCG	AGCGCGAGCA	GAGCTCAAGG	ATCGGCTCAA	GCCTGGCGGC	ACCAACCTCA	180

CCCAGGTCCT CAAGGACGCG GAGAGCGATG AAGTCTTGGG CAAAATGAAG GTGTCTGCGC	240
TGCTTGAGGC CTTGCCAAAG GTGGGCAAGG TCCAGGCGC	279

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACACGGTCGA ACTCGACGAG CCCCTCGTGG AGGTGTCGAC CGACAAGGTC GACACCGAAA	60
TCCCTCGCCG GCCGCGGGTG TGCTGACCAA GATCATCGCC CAAGAAGATG ACACGGTCGA	120
GGTCGGCGGC GAGCTCTCTG TCATTGGCGA CGCCCATGAT GCCGGCGAGG CCGCGGTCCC	180
GGCACCCAG AAAGTCTCTG CCGGCCAAC CCGAATCCA	219

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGCTGCCGA CATCGGCGCC GCGCCCGCCC CCAAGCCGCG ACCCAAGCCC GTCCCCGAGC	60
CAGCGCCGAC GCCGAAGGCC GAACCCGCAC CATCGCCGCC GGCGGCCAG CCAGCCGGTG	120
CGGCCGAGGG CGCACCGTAC GTGACGCCGC TGGTGCGAAA GCTGGCGTCG GAAAACAACA	180
TCGACCTCGC CGGGGTGACC GGCACCGGAG TGGGTGGTCG CATCCGCAA CAGGATGTGC	240
TGGCCGCGGC TGAACAAAAG AAGCGGGCGA AAGCACCGGC GCCGGCCGCC CAGGCCGCCG	300
CCGCGCCGCG CCCGAAAGCG CCGCTGAAG ATCCGATGCC GC	342

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GGGTCTTGGT CAGTATCAGC GCCGACGAGG ACGCCACGGT GCCCGTCGGC GGCGAGTTGG	60
CCCGGATCGG TGTCGCTGCC GACATCGGCG CCGCGCCCGC CCCCAAGCCC GCACCCAAGC	120
CCGTCCCGGA GCCAGCGCCG ACGCCGAAGG CCGAACCCGC ACCATCGCCG CCGGCGGCCG	180
AGCCAGCCGG TCGGCGCGAG GGCGCACCGT ACGTGACGCC GCTGGTGCGA AAGCTGGCGT	240

CGGAAAACAA CATCGACCTC GCCGGGGTGA CCGGCACCGG AGTGGGTGGT CGCATCCGCA	300
AACAGGATGT GCTGGCCGCG GCTGAACAAA AGAAGCGGGC GAAAGCACCG GCGCCCTGAG	360
CGCTTCATCA CCCGGTTAAC CAGCTTGCCC CAGAAGCCGG CTTGACCTC TTCGCGGGTC	420
TTGGTCCGCT GCAGGCGGTC GGCGAGCCAG TTCAGGTTAG GCGGCCGAAA TCTTCCAGTT	480
CGCCAGGAAG GGCACCCGGA ACAGGGTCCG CACCC	515

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CCGACCCCAA GGTGCAGATT CAACAGGCCA TTGAGGAAGC ACAGCGCACC CACCAAGCCG	60
TGACTCAACA GGCGGCGCAA GTGATCGGTA ACCAGCGTCA ATTGGAGATG CGACTCAACC	120
GACAGCTGGC GGACATCGAA AAGCTTCAGG TCAATGTGCG CCAAGCCCTG ACGCTGGCCG	180
ACCAGGCCAC CGCCGCCGGA GACGCTGCCA AGGCCACCGA ATACAACAAC GCCGCCGAGG	240
CGTTTCGAGC CCAGCTGGTG ACCGCCGAGC AGAGCGTCGA AGACCTCAAG ACGCTGCATG	300
ACCAGGCGCT TAGCGCCGCA GCTCAGGCCA AGAAGGCCGT CGAACGAAAT GCGATGGTGC	360
TGCAGCAGAA GATCGCCGAG CGAACCAAGC TGCTCAGCCA GCTCGAGCAG GCGAAGATGC	420
AGGAGCAGGT CAGCGCATCG TTGCGGTCGA TGACTGAGCT CGCCGCGCCA GGCAACACGC	480
CGAGCCTCGA CGAGGTGCGC GACAAGATCG AGCGTCGCTA CGCCAACGCG ATCGGTTCGG	540
CTGAACTTGC CGAGAGT	557

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CAGGATAGGT TTCGACATCC ACCTGGGTTT CGCACCCGGT GCGCGACCGT GTGATAGGCC	60
AGAGGTGGAC CTGCGCCGAC CGACGATCGA TCGAGGAGTC AACAGAAATG GCCTTCTCCG	120
TCCAGATGCC GGCACTCGGT GAGAGCGTCA CCGAGGGGAC GGTACCCGC TGGCTCAAAC	180
AGGAAGGCGA CACGGTCGAA CTCGACGAGC CCCTCGTGA GGT	223

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

AAGAAGTACA	TCTGCCGGTC	GATGTCGGCG	AACCACGGCA	GCCAACCGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATAACG	CCAGTCCCGG	CGCACAAACA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTC	GGCCTTGACG	180
CACGACTGTG	CGCCGAGCC	TGCAACGTCT	TGCTGGTCGA	TGGCGTACAG	CACCGGCCGC	240
AACGACATGG	GCCAGGTCCA	CGGTTTGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	300
GTCAGGCCCG	CGTGGAAGTG	GAACGCTTTG	GCGGTGTATT	GCCAGAGCGA	GCGCACGGCG	360
TCGGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	420
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCCAGCGCAT	ACCCGCTGGG	AAGCACGTCA	CGCCGCACTG	TTCCCAGCCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTCGCGC	CGCCACGTCA	ACGCCAGC			578

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ACAACGATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	60
ACGAGCAGCG	CGCGGCCCGG	TTGGAGAAGG	CTGTGCGCGC	ACGTCGAGCG	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCGGCACCA	ACCTCACCCA	GGTCCTCAAG	GACGCGGAGA	180
GCGATGAAGT	CTTGGGCAAA	ATGAAGGTGT	CTGCGCTGCT	TGAGGCCTTG	CCAAAGGTGG	240
GCAAGGTCAA	GGCGCAGGAG	ATCATGACCG	AGCTGGAAAT	TGCGCCCCAC	CCCGCCGCTT	300
TCGTGGCCTC	GGTGACGTC	AGCGCAAGGC	CCTGCTGGAA	AAGTTCGGCT	CCGCCTAACC	360
CCGCGGCCCG	ACGATGCGGG	CCGGAAGGCC	TGTGGTGGGC	GTACCCCGCG	ATACGGGGGA	420
GAAGCGGCCT	GACAGGGCCA	GCTCACAATT	CAGGCCGAAC	GCCCCGGTGG	GGGGGAACCC	480
GCCC						484

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AGGACTGGCA	CGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTC	GGCCTTGACG	60
CACGACTGTG	CGCCGAGCC	TGCAACGTCT	TGCTGGTCGA	TGGCGTACAG	CACCGGCCGC	120
AACGACATGG	GCCAGGTCCA	CGGTTTGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	180
GTCAGGCCCG	CGTGGAAGTG	GAACGCTTTG	GCGGTGTAGT	GCCAGAGCGA	GCGCACGGCG	240
TCGGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	300
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	360
CCCAGCGCAT	ACCCGCTGGG	AAGCACGTCA	CGCCGCACTG	TCCCAGCCA	CGGTCTTTGC	420

ACTTGGTACT GACGTCGCGC CGCCACGTCG AACGCCAGCG CCATCGCGCC GAAGAACAGC 480
 ACGAAGTACA CGCCGGACCA CTTGGTGGCG CAAGCCAATC CCAAGCAGCA CCCCGGC 537

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Gly	Gly	Ala	Ala	Ala	Gly	Gln	Gln	Ser	Asp	Val	His	Pro	Phe	Ala	Asn
1				5					10					15	
Leu	Ile	Ala	Val	Asp	Asp	Glu	Arg	Ala	Glu	Arg	Arg	Asp	Asp	Glu	Glu
			20					25					30		
Arg	Gln	Glu	Ala	Val	Gln	Gln	Arg	Gly	Pro	Arg	Gly	Asp	Glu	Ala	Asp
		35					40					45			
Pro	Val	Ala	Asp	Gln	Gln	His	Pro	Gly	Asp	Gly	Ala	Asp	Gln	Cys	Arg
		50				55					60				
Pro	Ala	Asp	Pro	Pro	His	Asp	Pro	His	His	Gln	Arg	His	Gln	Asp	His
65					70					75				80	
Thr	Gln	Gln	Gly	Ala	Gly	Glu	Pro	Pro	Ala	Glu	Ser	Val	Val	Thr	Glu
			85						90					95	
Asp	Gly	Leu	Pro	Asp	Arg	Asp	Gln	Leu	Leu	Thr	Asp	Arg	Arg	Val	Asn
		100						105					110		
His	Gln	Ala	Val	Pro	Gly	Val	Val	Phe	His	Pro	Met	Val	Val	Gln	His
		115					120					125			
Leu	Pro	Gly	Leu	Ala	Val	Arg									
		130				135									

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Gln	Lys	Tyr	Gly	Gly	Ser	Ser	Val	Ala	Asp	Ala	Glu	Arg	Ile	Arg	Arg
1				5					10					15	
Val	Ala	Glu	Arg	Ile	Val	Ala	Thr	Lys	Lys	Gln	Gly	Asn	Asp	Val	Val
			20					25					30		
Val	Val	Val	Ser	Ala	Met	Gly	Asp	Thr	Thr	Asp	Asp	Leu	Leu	Asp	Leu
		35				40						45			
Ala	Gln	Gln	Val	Cys	Pro	Ala	Pro	Pro	Pro	Arg	Glu	Leu	Asp	Met	Leu
		50				55					60				
Leu	Thr	Ala	Gly	Glu	Arg	Ile	Ser	Asn	Ala	Leu	Val	Ala	Met	Ala	Ile

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65          70          75          80
Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
      85          90          95
Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
      100        105        110
Pro Gly Arg Leu Gln Thr Ala Leu Glu Gly Arg Val Val Leu Val
      115        120        125
Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
      130        135        140
Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
145          150          155

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(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1          5          10          15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
      20        25        30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
      35        40        45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
      50        55        60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
63          70          75          80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
      85          90

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(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1          5          10          15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
      20        25        30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
      35        40        45

```

Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
 50 55 60
 Val Ser Ala Gly Pro Thr Arg Ile
 65 70

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1 5 10 15
 Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
 20 25 30
 Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
 35 40 45
 Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
 50 55 60
 Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu
 65 70 75 80
 Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
 85 90 95
 Gln Ala Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
 100 105 110
 Pro

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1 5 10 15
 Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
 20 25 30
 Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
 35 40 45
 Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala
 50 55 60
 Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser


```

65          70          75          80
Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
      85          90          95
Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Glu Gln Lys Lys Arg
      100          105          110
Ala Lys Ala Pro Ala Pro
      115

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1          5          10          15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
      20          25          30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
      35          40          45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
      50          55          60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
65          70          75          80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
      85          90          95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Ala Gln Ala Lys Lys Ala
      100          105          110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
      115          120          125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
      130          135          140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145          150          155          160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
      165          170          175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
      180          185

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
           20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
           35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
           50           55           60
Leu Asp Glu Pro Leu Val Glu
65           70

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
           20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
           35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
           50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
           65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
           85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
           100           105           110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
           115           120           125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
           130           135           140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
           145           150           155           160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
           165           170           175
Arg Ser Leu His Leu Val
           180

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Leu Glu Lys Ala Ala Ala
      20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
      35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
      50           55           60
Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
      65           70           75           80
Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
      85           90           95
Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
      100          105          110
Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
      115          120          125
Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
      130          135          140
Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
      145          150          155          160

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1           5           10           15
Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val
      20           25           30
Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
      35           40           45
Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
      50           55           60
Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
      65           70           75           80
Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
      85           90           95
Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
      100          105          110
Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His

```

```

      115              120              125
Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
      130              135              140
Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
      145              150              155              160
Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
      165              170              175
Pro Arg

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

ATGCCAAGCC GGTGCTGATG CCCGAGCTCG GCGAATCGGT GACCGAGGGG ACCGTCATTC      60
GTTGGCTGAA GAAGATCGGG GATTCGGTTC AGGTTGACGA GCCACTCGTG GAGGTGTCCA      120
CCGACAAGGT GGACACCGAG ATCCCGTCCC CGGTGGCTGG GGTCTTGGTC AGTATCAGCG      180
CCGACGAGGA CGCCACGGTG CCCGTCGGCG GCGAGTTGGC CCGGATCGGT GTCGCTGCCG      240
AGATCGGCGC CGCGCCCGCC CCCAAGCCCC C

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Ala Lys Pro Val Leu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly
  1              5              10              15
Thr Val Ile Arg Trp Leu Lys Lys Ile Gly Asp Ser Val Gln Val Asp
      20              25              30
Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro
      35              40              45
Ser Pro Val Ala Gly Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala
      50              55              60
Thr Val Pro Val Gly Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Glu
      65              70              75              80
Ile Gly Ala Ala Pro Ala Pro Lys Pro
      85

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAGGTAGCGG ATGGCCGGAG GAGCACCCCA GGACCGCGCC CGAACCGCGG GTGCCGGTCA 60
TCGATATGTG GGCACCGTTC GTTCCGTCCG CCGAGGTCAT TGACGAT 107

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GGCGCTTGTG 60
TTTCCTGCCT CGGTTGCCAG CGCAGATCCA CCTGACCCGC ATCAGCCGGA CATGACGAAA 120
GGCTATTGCC CGGGTGGCCG ATGGGGTTTT GCGGACTTGG CCGTGTGCGA CGGCGAGAAG 180
TACCCCGACG GCTCGTTTTG GCACCAGTGG ATGCAAACGT GGTTTACCGG CCCACAGTTT 240
TACTTCGATT GTGTACGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGTTTGC 300
GGTGGGGCAA TTCCGTCCGA GCAGCCCAAC GTCCTCTGA 339

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro

	85		90		95
Pro Gly Gly Cys Gly Gly Ala Ile	Pro Ser Glu Gln Pro Asn Ala Pro				
100	105		110		

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GTGACCACGG TGGGCCTGCC ACCAACCCGG GCAGCGGCAG CCGCGGCGGC GCCGGCGGCT	60
CCGGCGGCAA CGGTGGCGCC GGGGGTAACG CCACCGGCTC AGGCGGCAAG GGCGGCGCCG	120
GTGGCAATGG CGGTGATGGG AGCTTCGGCG CTACCAGCGG CCCCCTCTCC ATCGGGGTCA	180
CGGGCGCCCC CGGCGGCAAC GGCGGCAAGG GCGGCGCCGG TGGCAGCAAC CCCAACGGCT	240
CAGGTGGCGA CGGCGGCAAA GGCGGCAACG GCGGTGCCGG CGGCAACGGG GGCTCGATCG	300
GCGCCAACAG CGGCATCGTC GCGGTTCCG GTGGGGCCGG TGGCGCTGGC GGCGCCGGCG	360
GAAACGGCAG C	371

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GTCCGGGTCC CACCACCGCG CCGGCGCGCC CCTAGCGGCC GGGCGCACCA GCCCCTTTTC	60
TTGACTCGTT CAAGAAAAGG GCCTTCTGTT TGGTCGGCCA TGTTGGCATG ATCGTGACCC	120
ATGGGCAACA TCGACGTCGA CATCTCGGCC AAGGTCTAGC TCCATGCGAA TCGCCGCCGC	180
GGTGGTGAGC ATCGGTCTAG CCGTCATAGC AGGGTTCGCG GTACCTGTTG CCGACGCACA	240
CCCCTCGGAG CCCGGGGTTG TGTCTACGC GGTGCTCGGA AAGGGGTCGG TCGGCAACAT	300
CGTCGGCGCC CCAATGGGGT GGGAGGCGGT GTTCACCAAG CCGTTCAGG CGTTTTGGGT	360
CGAACTACCG GCGTGCAACA ACTGGGTGGA CATCGGGCTG CCCGAGGTGT ACGACGATCC	420
CGAC	424

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GCGATGGCGG	CCGCGGGTAC	CACCGCCAAT	GTGGAACGGT	TTCCCAACCC	CAACGATCCT	60
TTGCATCTGG	CGTCAATTGA	CTTCAGCCCG	GCCGATTTCG	TCACCGAGGG	CCACCGTCTA	120
AGGGCGGATG	CGATCCTACT	GCGCCGTACC	GACCGGCTGC	CTTTCGCCGA	GCCGCCGGAT	180
TGGGACTTGG	TGAGTCGCA	GTTGCGCAG	ACCGTCACCG	CCGACACGGT	GCGCATCGAC	240
GTCATCGCCG	ACGATATGCG	TCCCGAACTG	GCGGCGGCGT	CCAAACTCAC	CGAATCGCTG	300
CGGCTCTACG	ATTGCTC					317

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGGCGTATGC	GCTTCGCAGC	CGGTGCCGCG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTCGATCAGC	ATCGCACTGT	GCCGTCTGTC	ACCGACACCG	CCGTCCAACG	120
TGAACTGAGG	GCGGAAAATC	GGCCGAAATC	TGCCCCCTCAG	TTCACGCTCG	GCGCCTAACG	180
GTTCTGGAAG	TTGGGTGCGC	GCTTCTCGGC	GAACGCGCGC	GGGCCTTCCT	TGGCGTCGTC	240
GGACAGGAAG	ACCTTGATGC	CGATCTGGGT	GTCGATCTTG	AACGCCTCGT	TTTCGGGCAT	300
GCACTCGGTC	TCGCGGATGG	ACCGCAAGAT	GGCCTGCACG	GCCAGGGGTC	CGTTAGCCGA	360
GATGGCGTCG	GCAAGTTCTA	GAACCTTGGT	CAACGCCTGG	CCGTCGGGCA	CACGTGGCCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GCGTGCCGCT	GAACACCAGC	CCGCGGCTGC	CAGATCTCCC	GGACTCGGTA	GTGCCGCCCG	60
TGGCGTCGTT	GCTCTCCTGA	CGGGGCGCGG	CGACCATAAG	GTCGCTAATG	CCCAGGTAGC	120
GGCCCAGGTG	CATGGAGTCG	ATGATGATGC	GACTCTCCAG	CTCGCCGACC	GGGAGCTTGG	180
CATCGGGCCT	GATCAGCCAG	GACGCGTAGG	ACAAGTCGAT	CGAATGCATA	GTGGCCTCCA	240
GAGTGGCCGT	GCCACTTCCG	GCGTGCTCCA	CGGCAAATGC	CTTGATTCTT	AGCTCCGCGT	300
AGTGTTCCTG	CATCGCCTGC	GGGATGAATG	GGAACCGCAG	GATGGCGACA	AACGGGTCTG	360
ACCTCAGGTT	TGCCGCTTTG	CGCACAGTGG	TCGACAGCCG	GTACTCGGCA	TAAATGCTGG	420
CCCCGA						426

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

AGACCGGCGA GGGTGTGGTC GCTGCCCCGG GCATTGTCGA TAATCTGCGC TGGGTGCGACG	60
CGCCGATCAA CTAGTGAGGC GCAACGCTAG GCTTTGGGAT ACCCACAGCT AAAAAGTTTA	120
TCAAAGAAAC GAAGAAGGTT GCCATGAGCA CTGTTGCCGC CTACGCCGCC ATGTGCGGCGA	180
CCGAACCCCT GACCAAGACC ACGATCACCC GTCGCGACCC GGGCCCCGAC GACATGGCGA	240
TCGACATCAA ATTCGCCGGA ATCTGTCGCT CGGACATCCA TACCGTCCAA ACCGAATGGG	300
GGCAACCGAA TTTACCTGTG GTCCCTG	327

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly	
1 5 10 15	
Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly	
20 25 30	
Ser Gly Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe	
35 40 45	
Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly	
50 55 60	
Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser	
65 70 75 80	
Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly	
85 90 95	
Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala	
100 105 110	
Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:


```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1           5           10           15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
          20           25           30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
          35           40           45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
          50           55           60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
65           70           75           80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ser Lys Leu Thr
          85           90           95
Glu Ser Leu Arg Leu Tyr Asp Ser
          100

```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
 1           5           10           15
Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
          20           25           30
Ala Pro Thr Pro Pro Ser Asn Val Asn
          35           40

```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
 1           5           10           15
Val Pro Pro Val Ala Ser Leu Leu Ser
          20           25

```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
 1             5             10             15
Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
      20             25             30
Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
      35             40             45
Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

GCTTGGAGCC CTGGAGCGAC GGTGTGGGTC TGGGGGTCGA TTCGTTCTCG GCGAAAGTCA      60
ACTAAAGACC ACGTTGACAC CCAACCGGCG GCCCGGCATG GGCCGTCGCG GCGTAGAAGC      120
TTTGACCGCG GCGCGAAACG TTCGCTGCTG CGGCCCATGC AGATCGCACA CGCTTGCTTG      180
AACATCGGGT GGAGCCGGTG GTAACGCCAG GCT                                213

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

CCGAGCTGCT GTTCGGCGCC GGCGGTGCGG GCGGCGCGGG TGGGGCGGGC ACCGACGGCG      60
GGCCCCGGTGC TACCGGCGGG ACCGGCGGAC ACGGCGGAGT CGGCGGCGAC GGCGGATGGC      120
TGGCACCCCGG CGGGGCCCGG GGGGCCGCGG GGCAAGGCGG GGCAGGTGGT GCCCGCAGCG      180
ATGGTGGCGC GTTGGGTGGT ACCGGCGGGA CGGGCGGTAC CGGCGGCGCC GGTGGCGCCG      240
GCGGTGCGCG CACACTGCTG CTGGGCGCTG GCGGACAGGG CGGCCTCGGC GGCGCCGGCG      300
GACAAGGCGG CACCGGCGGG GGCGGCGGA GATGGCGTTC TGGGGGGTGT CAGTGGCACT      360
GGTGGTA                                367

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

AAGGCGTGAT	TGGCAAGGCG	ACCGCGCAGC	GGCCCGTAGC	CGCGGGACGG	CCCAGGCCCC	60
GACCGCAGCG	GCCGGTGTCT	GACCGGGTCA	GCGACCAGCG	GCGCTGACCG	TGCCGCTCGT	120
CTACTTCGAC	GCCAGCGCCT	TCGTCAAAC	TCTCACCACC	GAGACAGGGA	GCTCGCTGGC	180
GTCCGCTCTA	TGGGACGGCT	GCGACGCCGC	ATTGTCCAAC	CGCCTGGCCT	ACCCCGAAGT	240
CCGCGCCGCA	CTCGTGCAA	CGGGCCGCAA	TCACGACCTA	ACCGAATCCG	AGCTCGCCGA	300
CGCCGAGCGT	GACTGGGAGG	ACTTCTGGGC	CGCACCCGCC	CAGTCGAAC	CACCGCGACG	360
GTTGAACAGC	ACGCCGGGCA	CCTCGCCCCG	ACACATGCCT	TACGCGGAGC	CGACACCGTT	420

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

CTCTTGTGTCGG	TGGCATCGGC	GGTACCGGCG	GAACCGGCGG	CAACGCCCGGT	ATGCTCGCCG	60
GCGCCGCCCG	GGCCGGCGGT	GCCGGCGGGT	TCAGTTTCAG	CACTGCCCGGT	GGGGTGGCG	120
GCGCCGGCGG	GGCCGGTGGG	CTGTTTACCA	CCGGCGGTGT	CGGCGGCCG	GGTGGGCAGG	180
GTCACACGGG	CGGGGCGGGC	GGCGCCGGCG	GGGCCGGCGG	GTTGTTTTGT	GCCGCGGCA	240
TGGGCGGGGC	GGGCGGATTC	GGGGATCACG	GAACGCTCGG	CACCGGCGGG	GCCGCGGGG	299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser
1 5 10 15
Ala Lys Val Asn
20

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
 1             5             10             15
Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly
      20             25             30
Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
      35             40             45
Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
      50             55             60
Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
      65             70             75             80
Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
      85             90             95
Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Arg Arg Arg Trp Arg
      100            105            110
Ser Gly Gly Cys Gln Trp His Trp Trp
      115            120

```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1             5             10             15
Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
      20             25             30
Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1             5             10             15
Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
      20             25             30
Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Leu Phe
      35             40             45
Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50             55             60
Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
65             70             75             80
Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
      85             90             95
Ala Gly Gly

```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

TCCTGTTCCG CGCCGGCGGG GTGGGCGGTG TTGGCGGTGA CGGTGTGGCA TTCCTGGGCA      60
CCGCCCCCGG CGGGCCCGGT GGTGCCGCGG GGGCCCGTGG GCTGTTTCAGC GTCGGTGGGG      120
CCGGCCGGCG CGGCGGAATC GGATTGGTCG GGAACAGCGG TGCCGGGGGG TCCGGCGGGT      180
CCGCCCTGCT CTGGGGCGAC GGCGGTGCCG GCGGCGCGGG TGGGGTCGGG TCCACTACCG      240
GCGGTGCCCG CGGGGCGGGC GGCAACGCCA GCCTGCTGGT AA                          282

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

CGGCACGAGC CGTGCTACTG GTCAACTGAT GCCCTGATTG TGACCTTCCC GCGCCCGGAT      60
CAGTGCTTCT CAGGACCGAC GTAATATTCG AAAACCAATC CGGCCGCCGA GGCGAGGATG      120
AATGCCACAC CGGCGGCGAT CAGCCACGGG AGCCACAACG CGATGCCGAC CGCTGCCACC      180
GAGCCGGACA ACGCGACCAT GATCGGCCAC CAGCTATGCG GACTGAAGAA TCCAAGTTCT      240
CCTGCGCCGT CGCTGATTTC AGCGCCTTCG TAGTCCTCGG GCCGGGAATC TAACCGGCGG      300
GCCACAAACC GGAAGAAGGT GGCGACGATC AACGCCATGC CGCCGGTGAG CGCCAACGCA      360

```

ATGGTGCCAG CCCACTCGAC ACCACCGGTG GCGAACATCG AGGTCAACAC GCCGT 415

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TCACCGCGTG AACGGTTCGT AACACTGATA CGTATGCTTG TCAGCGAGCA GATCAAGTCC	60
AGTCCGACCA ATGCCAGGAG ATCATCGGCT AGGCTCACGG TTTCGCCTGG GACGAGACGG	120
TATTGAGTTC TGGCGTTGGA CGGTCCGTGG CGTGGTGGGA AGTCTGACGC GGCATCAGAA	180
CGGTTGTCAA TACCAGTCTT TGGGGGATAT GGCCTATTTG GTGTCGTCGG GCCGCTCCAC	240
CGGATCCCTT TTCGAACGTT GCGCAAGCGC GGTCCAGTTA CGGCCTGTTC ACTGCGCGCT	300
GGCGTAGCTG CGCGGCCTCG ATCGGTTTGA ACGTCATCGC AATCCCCGCA ATGGGTGAGT	360
ACCTGACGCT CCT	373

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CCAAACCGGA CAGGCCGGCA GCGACGGTCG GAAGTTGCAC CACGGTGCGC GCTCCATGTA	60
GCCAACCGGT GACCACGGCG TAGACAGCAG ATCCGTGGAT CGCGCGTTCC GTGTCGTCCG	120
GGCCGAGTAC CCGCGGGCCG AACCGCAGCG ACCAAAGCAA CGCGATCGAT ACGGGGATCG	180
CCACTCGTGC CGAATTCGAG CTCCGTGCGC AAGCTTGCGG CCGCACTCGA ACCCGGGTGA	240
ATGATTGAGT TTAAACCGCT TAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAAACGGG	300
TCTTGAGGGG TTTTGTGCTG AAAGGAGGAA CTATATCCGG ATAACCTGGC GTAGTAGCGA	360
AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGACGCG	420
CCC	423

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

AGTGGCCAGC	CGGTCCGCCA	ATGCATCCAG	CTCCCGGTAC	GTCAGCTGAC	CATCCGCCCA	60
ACTGACCGCC	ACCGAGTCAG	GCTGTGCCGC	AGCGATTTTCG	GCGAACCGGG	TATGCACCGC	120
GGGTGCCGAC	GTCGTCACAT	CCGGCAGGCC	GGGTGCCGTC	GGATCGTGCT	CGCCGTCCAG	180
CAGAATGTCG	ACGTCCGCA	GCGGCCGATC	CCACCGGCTG	ACCAAGCGCT	GTAACACAGC	240
CAGCACCCGC	CTGCCGAGGC	TTTCGGGCGC	CATCGTGCCC	AGCGCACCGT	CGAGCACCTC	300
CACTAGCAGC	GTGAGCTCAC	CGGTGCTGCG	GTGCGCGGCG	ACGGTCACCG	GAAAGTGCGA	360
CAAACCTCTCT	AGCGCCACCG	GACGGAACGT	CACCCCGTTT	GCGA		404

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GTCTTGCTCG	CAGGCTGTTT	TTTGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCCC	60
ACCATCGAAC	CCGCCCAACC	GGCGGTGTCA	CCGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTTCG	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCGC	CGATTCCGGC	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGCGCGT	CAATTTTCTG	CCGGGCCCCG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCCT	TGCCGCCCGC	GGCGGCTACT	TCGTGGCCGA	CCTGTCTCTC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

ATGCATATCA	CGCTCAACGC	CATCCTGCGT	GCGATCTTCG	GGGCCGGCGG	CAGTGAACCTA	60
GACGAGCTGC	GCCGCCTCAT	TCCGCCGTGG	GTACGCTGG	GCTCGGCCT	GGCGGCGCTA	120
CCGAAACCCA	AACGCGACTA	TGGCCGCCTT	AGCCCGTGGG	GCCGGCTGGC	CGAGTGGCGG	180
CGCCAGTACG	ACACTGTTCAT	CGACGAGCTC	ATCGAAGCCG	AGCGGGCCGA	CCCGAACTTC	240
GCCGATCGGA	CCGACGTTTT	GGCGTTGATG	CTGCGCAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTGCGCGA	AGGACATTGG	CGACGAACTG	CTCACGCTGC	TTGCCGCCGG	GCACGAAACC	360
ACGGCGGGCGA	CATGGGCTGG	GCGTTCGAAC	GGCTCAACCG	GCACCCCGAC	GTGCTCGCGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GTCCTGGTCG	CAGGCTGTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCCC	60
ACCATCGAAC	CCGCCCAACC	GGCGGTGTCA	CCGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCG	ACAACGGCAC	CGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCG	CGATTCGGCG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCCG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCCT	TGCCGCCCCG	GGCGGCTACT	TCGTGGCCGA	CCTGTCTCTC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420
CGCCGCTCCG	ACGGCAAGCT	GGTGCTGGGC	AGCGCAGATG	GCGCCGTCTA	CACGCTTGCC	480
AAGAACCCGC	AGTTGACCGG	CGTCGGCGCC	GCCACCGTAG	CC		522

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GCTGGGGCGC	ACCGCCGTCC	GGCGGCCCCA	GGCCCTGGGC	CCAGACCCCG	CGCAAAACCA	60
ACCCGTGGCC	CTTAGTGGCC	GGCGCCGCGG	CCGTCTGTGCT	CGTCCTCGTG	TTGGGCGCCA	120
TCGGCATCTG	GATCGCCATC	CGGCCCAAGC	CGGTACAGCC	GCCTCAGCCG	GTTGCGGAGG	180
AGCGCCTTAG	CGCCCTACTG	CTGAATCCTT	CAGAAGTCAA	CGCCGTGATG	GGCTCGTCGT	240
CCATGCAGCC	GGGCAAACCG	ATCACATCGA	TGGACTCTTC	GCCGGTGACG	GTGTCCCTGC	300
CGGACTGCCA	GGGCGCGCTG	TATACCAAGC	AGGATCCGGT	GTATGCCGGC	ACCGGCTACA	360
CCGCCATCAA	CGGCCTTGATT	TCATCCGAGC	CGGGCGACAA	CTACGAACAT	TGGGTGAACC	420
AAGCCGTCGT	CGCCTTTCCG	ACCGCCGACA	AAGCCCGCGC	GTTCGTGCAG	ACTTCGGCCG	480
ACAAATGGAA	GAAGTGCACA	GGCAAGACGG	TCACCGTCAC	GAATAAGGCC	AAGACCTACC	540
GGTGGACGTT	TGCCGACGTC	AAAGGCAGCC	CGCCGACGAT	CACGGTGATA	GACACCCAAG	600
AAGGCGCTGA	GGGCTGGGAA	TGCCAACGCG	CGATGAGCGT	GGCCAACAAT	GTGGTTGTTC	660
ACGTCAACGC	ATGCGGGTAC	CAGATCACCA	ATCAAGCAGG	CCAGATCGCC	GCCAAGATCT	720
GTTGACAAAG	TCAACAAGG					739

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGACGTCGTC GAGGCCGCCA TCGCCCGCGC CGAAGCCGTT AACCCGGCAC TGAACGCGTT 60
GGCGTATGC 69

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

ACTGCACCCG GCAGGCGCGA CCAACGGATC GGGTCAACTA GCACTGCCGG TGGAGGCGCC 60
CCCGCGGTCT GTGCCTTCCC ACGGGGAACC CTTGGGCAGC GCGGCTCCAG AAGGGTTGGA 120
GGGAGAGTTC GACGACCGTA TCGACGAGCG GTTCCCGGTC TTCAGCTCSG CCAGTCTCGC 180
CGAAGCGCTG CCGGGTCCGC TGACCCCGAT GACGCTGGAT GTCCAGTTGA GTGGACTGCG 240
CGCGGCCCGT CCGGCGATGG GTCGGGTACT GCGGCTTGGC GGTGTCGTTG CCGATGAGTG 300
GGAGAGAAGA GCCATCGCGG GTTTCGGTCA CCGCCCGTAT ATCGGAGTGT CCGCCAATAT 360
TGTGGCCGCC GCCCAACTGC CGGGGTGGGA CGCGCAGGCC GTAACCCGGC GGGCACTGGG 420
CGAGCAACCG CAGGTCATG AGCTGCTTCC GTTTGGTCTG CCGCAACTTG CCGGCGGACC 480
GCTCGGCTCG GTCGCGAAGG TGGTCGTGAC GGCACGGTCT CTG 523

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GTGTCGGTGT CGTCGGGGTA GGAGCGACTT CCCCAGCCGG CGCCGGCGCC GGAGCGGGCT 60
CTGCAGGAAC CCGTGCCGGC GCCGGCGGCG GGGCGACCAA AGGCCGGATC GATTCCGGCA 120
GCGCCTTGCC CGCGCCCTTG TCCACCGGGT TGTGGCGGT CCCGAGCCAT ACCACAAACC 180
AACGCTGAAG GGGCCCGGCG TCCGGTGCCT TCGCCCGGG CGAC 224

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TGAACTGACT GCCCGGCTCG ATCGGCGGCG GCGGCGTGTC ATAGCTGCGC CGCCAGGCCA 60

TGAACTGCTC	TTCGCCATAG	CGGGCCTTGG	TCTCGGCCTT	GTCCAAACCC	TGCAGCGCGC	120
CGTAGTGGCG	TTCGTTGAGC	CGCCAGCTAC	GCCGCACGGG	AATCCAGAGC	CGATCGGCGC	180
TGTCCAACGC	CAGATGCGCG	GTGGTGATCG	CGCGCCGCAG	CAACGAGGTG	TAGAGCACGT	240
CGGGCAATAG	GTCGTGTTCC	GCGATCAGCT	CGCCGCTTCG	AACCGCCTCT	GCCTGGCCCT	300
TGTCCGTGAG	GCCGACATCG	ACCCAGCCGG	TGAACAGGTT	GAGGGCATTG	CAGTCGCTCT	360
CGCCGTGGCG	CAGCAACACC	AGGCTGCCAG	TGTTTGCCAT	ACCGGCAAGT	CTCTCACGCA	420
CTCCCGCACT	CCTCATCGTG	GACCAAAATG	CCCGAATTCT	CCTCGGTCCG	CTGCGCAGCG	480
CGTTCATACC	GCCGAGGTGG	TCGGCACCGT	AACGGCCGGT	T		521

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

CTCCAGGCTC	ATTCGCTCGA	ACAAAGCCAC	CCGGCCGTAC	AGCGGACGCC	CCCATTGCTT	60
GTCGTGATAG	TCGCGGTACA	GCTGGGCATC	GGGCCCTGGA	CGAACCTCCG	CCCAGGGGCA	120
GCGAACCAGC	CCGTCGCCGC	TCACGCGGGG	TCAGAACGGT	AGTGACAGAC	AGTCTCGCCG	180
CGCGAAGGGT	TTGACGCGTC	AGACTCGGCC	TCGGCGTCTT	CCGACGAGGC	GTGGATCGCC	240
CCGAGCTGAG	AGCGTAGCGC	CTCGAGCTCA	CGGCCGAGCC	GTTCCAGCAC	CCAGTCCACC	300
TCGCTGGTCT	TGTTCCCGCG	CAGCACCTGC	GTGAACTTGA	CCGCGTCGAC	ATCGGCGCGG	360
GTGACCCCGA	ACGCCGGCAG	CGTCGTCGCC	GTGTCGCCCC	GCGGCAGGGG	CGGCAACTGC	420
TCGCCA						426

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GCGGACACGG	CGGACAAAGC	GCAATCGGCC	TCGGCGGCGG	CGCCGGCGGC	GACGGGGGGC	60
AGGGCGGCGC	CGGCCGCGGA	CTGTGGGGTA	CTGGCGGCGC	CGGCCGACAC	GGCGGGGCAA	120
GGCGGTGGTA	CCGGGGGCCC	ACCGCTGCCC	GGTCAGGCAG	GCATGGGCGC	CGCGGTGGC	180
CCCGGTGGGC	TGATCGGCAA	CGGCCGGGCC	GGCGGCGAC			219

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

AAGATCATCG GCGCCGCTCC TTAGCATCGC TCGCCTCTGC ATCGTCGCCG GCGCGGATCA    60
CGGAGGTCCG GCCTTGTTACC CCACTCCTCG AACGGTCAGC ACCACAGTCG GGTTCCTCGG    120
ATCCTTTTCG ACCTTGGCCC GCAGACGCTG GACATGCACG TTCACCAGCC TGGTATCGGC    180
TGGGTGCCGG TAACCCCATC CCTGTTTCGAG CAGCACATCA CGAGTAAACA CCTGGCGCGG    240
CTTGCGCGCC AATGCGACCA ACAGGTCGAA TTCCAGCGGT GTCAACGAGA TCTGCTCACC    300
GTTGCGAGTG ACCTTGTTGCG CCGGTACGTC GATTTCTACG TCGGCGATGG ACAGCATCTC    360
GGCGGGTTTCG TCGTCGTTGC GGCGCAGCCG CGCCCGCACC CGCGCAACCA GCTCCTTGGG    420
CTTGAACGGC TTCATGATGT AGTCGTCGGC GCCCGACTCC AGACCCAGCA CCACATCCAC    480
GGTGTCCGTC TTTGCGGTGA GCATCACGAT CGGAACACCG GAATCGGCGC GCAACACCCG    540
GCACACGTCG ATGCCGTTCA TACCGGGGCA A

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1             5             10             15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
      20             25             30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
      35             40             45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
      50             55             60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
      65             70             75             80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
      85             90

```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1             5             10             15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro

```

20

25

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1               5               10               15
Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
      20               25

```

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1               5               10               15
His Pro Pro Asn
      20

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1               5               10               15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
      20               25               30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
      35               40               45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg

```

```

      50              55              60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
65              70              75              80
Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
      85              90              95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
      100             105             110
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
      115             120             125
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
      130             135             140

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1              5              10              15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
      20              25              30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
      35              40              45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
      50              55              60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
65              70              75              80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
      85              90              95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
      100             105             110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
      115             120             125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
      130             135             140

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
          20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
          35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
          85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
          100          105          110
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
          115          120          125
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
          130          135          140
Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
145          150          155          160
Lys Asn Pro

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1           5           10           15
Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Ala Val Val
          20           25           30
Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
          35           40           45
Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50           55           60
Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
65           70           75           80
Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
          85           90           95
Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
          100          105          110
Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
          115          120          125
Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
          130          135          140
Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
145          150          155          160

```

```

Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
      165                      170                      175
Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
      180                      185                      190
Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
      195                      200                      205
Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
      210                      215                      220
Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
      225                      230                      235                      240

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1              5              10              15
Leu Asn Ala Leu Ala Tyr
      20

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1              5              10              15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
      20              25              30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
      35              40              45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
      50              55              60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
      65              70              75              80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
      85              90              95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
      100             105             110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Ala Gln Leu Pro Gly

```

115	120	125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln		
130	135	140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro		
145	150	155
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu		160
165	170	

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala		
1	5	10
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr		
20	25	30
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr		
35	40	45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg		
50	55	60

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp		
1	5	10
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr		
20	25	30
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu		
35	40	45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala		
50	55	60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile		
65	70	75
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu		
85	90	95
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln		
100	105	110

Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Pro Ile Glu
 115 120 125
 Arg Gly Ser Gln Phe
 130

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1 5 10 15
 Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
 20 25 30
 Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg
 35 40 45
 Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1 5 10 15
 Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
 20 25 30
 Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
 35 40 45
 Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50 55 60
 Arg Gln Arg Arg Gly Arg Arg Arg
 65 70

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
      20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
      35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
      50           55           60
Pro Ile Pro Val Arg Ala Ala His His Glu
      65           70

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

CCGCACGTAA CACCGTGAAT TGAAGGGAGC CGCTGGTCAT GGGCCGATTC TATCCGTGGG      60
CGAACGGTTA TTGACGGCCC GGAGGCCACT CCGCTGCCAC CAAGTGGTGA CTCAGCGCGT      120
TTTCACGGCA ACGAACGGCG GACACACCAC TTGACATTCC ACAGCACGGC CGCG              174

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

TCGCAAACGG GGTGACGTTT CGTCCGGTGG CGCTAGAGAG TTGTGCGCAC TTTCCGGTGA      60
CCGTGCGCGC GCACCGCAGC ACCGGTGAGC TCACGCTGCT AGTGAGGTG CTCGACGGTG      120
CGCTGGGCAC GATGGCGCCC GAAAGCCTCG GCAGGCGGGT GCTGGCTGTG TTACAGCGCT      180
TGGTCAGCCG GTGGGATCGG CCGCTGCGCG ACGTCGACAT TCTGCTGGAC GGCGAGCACG      240
ATCCGACCGC ACCCGGCCTG CCGGATGTGA CGACGTCGGC ACCCGCGGTG CATAACCGGT      300
TCGCCGAAAT CGCTGCGGCA CAGCCTGACT CGGTGGCGGT CAGTTGGGCG GATGGTCAGC      360
TGACGTACCG GGAGCTGGAT GCATTGGCCG ACCGGCTGGC CACT              404

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His
 1           5           10           15
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu
          20           25           30
Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
          35           40           45
Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
          50           55           60
Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
65           70           75           80
Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
          85           90           95
His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
          100          105          110
Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
          115          120          125
Ala Asp Arg Leu Ala Thr
          130

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

GCTTCGACGG CTACGAGTAC CTGTTCTGGG TGGGTTGTGC GGGCGCCTAC GACGACAAGG      60
CCAAGAAGAC CACCAAGGCC GTCGCCGAGC TGTTCCGCGT CGCCGGGGTG AAATACTTGG      120
TGCTGGGCGC TGGGGAACCC TGCAACGGCG ACTCGGCGCG CCGCTCCGGC AACGAGTTCC      180
TCTTCCAGCA GCTGGCACAA CAGGCCGTCG AGACCCTGGA CGGTTTGTTT GAGGGTGTGG      240
AGACCGTCGA CCGCAAGATC GTTGTACCT GCGGCACTG CTTCAACACC ATCGGCAAGG      300
AATATCGGCA GCTGGGCGCC AACTACACCG TGCTGCACCA CACCCAGCTG CTCAATCGGT      360
TGGTGCGCGA CAAGAGGCTG GTCCCTGTCA CTCCGGTTTC TCAGGACATC ACCTACCACG      420
ACCCGTGCTA CCTGGGTCGG CACAACAAGG TCTACGAGGC ACCACGGGAG CTGATCGGTG      480
CCGCGGGGGC CACCTGAGCC GAGATGCCGC GCCATGCCGA CCGCAG                      526

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTCGCCGCCG TGATCTGGCC GGCGAACTTC GTCAGTGCAT CCAGACCCCA ACGATCATCG	60
ATCAGGCCGA TGCCCATGAT CACCGCACCG GCCACCAGCA CCGCGGGCAT GCCGGTGGAA	120
TAGACGAACC CCCGGGTGAG TGCCGGAAGC TGGGAGGCAA GAAAGACGGC GCCGACAATG	180
CCCAGGAACA TCGCCAACCC ACCCATCCGA GGGGTAGGCG TGACGTGCAC ATCTCGCTCC	240
CGCGGGTAGG CGACGGCTCC CAGGCGACTG GCCAGCATCC GCACCGGACC GGTCCGAAAA	300
TAGGTGATGA TCGCCGCGGT CAGCCCGACC AGCGCAAGCT CACGCAGCGG GACACCGGCG	360
CCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAACGCCGG CCACATCGCT GGACACCTCG	420
AGACCGTACT GCACCAACCT GAAGAGCTGA AACTCGCCG AACGTGCAAC AGCTGCGAAC	480
AATTGGG	487

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ACGAAGCGCG AGAATATGAG CCGGGGCAAC CCGGCATGTA CGAGCTTGAG TTCCCGGCGC	60
CTCAGCTGTC GTCGTCCGAC GGCCGTGGTC CCGGTGTTGGT GCACGCTTG GAAGGTTTCT	120
CCGACGCCGG CCATGCGATC CGCTGGCCG CCGCCACCT CAAGGCGGCC CTGGACACAG	180
AGCTGGTCCG GTCCTTCGCG ATCGATGAAC TACTGGACTA CCGCTCGCGG CGGCCATTAA	240
TGACTTTCAA GACCGATCAT TTCACCCACT CCGATGATCC TGAGCTAAGC CTGTATGCGC	300
TGCGCGACAG CATCGGCACC CCATTTCTGC TGCTGGCCGG TTTGGAGCCG GACCTGAAGT	360
GGGAGCGGTT CATCACCGCC GTCCGATTGC TGGCCGAGCG CCTGGGTGTA CGGCAGAACC	420
ATCGGCCTGG GCACCGTCCC GATGGCCGTT CCGCACACAC GACCGATCAC GATGACCGCT	480
CATTCCAACA ACCGGGAGCT ATCTCCGATT TTCAACCGTT CGATCTCC	528

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCAAGCCCGT CAAGGAGCCG GTGCCGGCCT TGCTCCGGT GCCGCCGACG CCGGCGTTGC	60
CGCCGTTGCC GCCGTTGCCG CCGGTACCGG GGTTCCTAC GGTGCCGCCG CCCGGCAGCA	120
TGGCCCGCCT GTTTAGGCCG TTTTCGCCG CCGCCCGTC ACCGGCTTG CCGCCATCGC	180

```

CGCCGTTGCC GCGCTGGTG GGGGTGGCGG CCTGGTTGAC GTATTGTTCC ACCGGCCCGG 240
CCCTTGACCC TTGGGCGGTG TCGATCGCGG CGTCGATGGA TCCGCCGACC ACGACGTGCG 300
AAGCCTCGCC TGCCGCCGCA GCGCCCAAC TGTGTGCGCG CTCCTGCGAT TTGGCCCCGG 360
CCGACGAGAT GATGGGCACC ACCGGAGCCT GCGGCCGTCT GGGGGAGGCC AGCGCGGGTT 420
CGCGGTCACG CCATACGCGA CGGTGCGCCG CCGCTTCGGA GATTTCAGG CTGCGTTGCA 480
CCAGATCGAG CAGCGGTGTG CCCAGGGACT GGGTTAGCCC GTTGGCGCCG CCGTTGTAGC 540
GGCGAGCGCA ATATCGGTGC CCACTCGACC CAACCGCGAC TCCATAAGCG ACACCATTGC 600
CGGTTGATGC 610

```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
 1           5           10           15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
 20           25           30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
 35           40           45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
 50           55           60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
 65           70           75           80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
 85           90           95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
100           105           110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
115           120           125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
130           135           140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
145           150           155           160
Ala Gly Ala Thr

```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1           5           10           15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20           25           30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35           40           45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
 50           55           60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65           70           75           80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85           90           95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys
 100          105          110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala
 115          120          125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
 130          135          140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln
 145          150          155          160
Leu

```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu
 1           5           10           15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
 20           25           30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
 35           40           45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
 50           55           60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
 65           70           75           80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
 85           90           95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Leu Ala
 100          105          110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
 115          120          125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
 130          135          140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser

```

145 150 155 160
 Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu
 165 170 175

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1 5 10 15
 Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
 20 25 30
 Thr Val Pro Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
 35 40 45
 Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
 50 55 60
 Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
 65 70 75 80
 Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
 85 90 95
 Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg
 100 105 110
 Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
 115 120 125
 Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
 130 135 140
 Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
 145 150 155 160
 Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
 165 170 175
 Pro Leu

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

AATTCGGCAC GARGAGCACC AACACCGGCT TCTTCAACTC CGGCGACGTC AATACCGGTA 60
 TCGGCAACAC CGGCAGCTTC AACACCGGCA GCTTCAATCC GGGCGATTCC AACACCGGGG 120

ATTTCAACCC	ANGCAGCTAC	CACACGGGGA	CTCGGAAACA	CCGGCGATTT	TACACCGGCS	180
CCTTCATCTC	CGGCAGCTAC	AGCAACGGGT	CTTGTGGAGT	GGAAATTATC	AGGGCTCATT	240
GGNTGCACCC	GGSCITRCGA	ATCCCTCGKG	CCAATTCAAC	TCCTCNACAA	GCTTGC3GCC	300
GCACTCSAGC	CCGGGTGAAT	GATTGAGTTT	AACCGCTNAN	CAATAACTAG	CATAACCCCT	360
TKGGGCCTCT	AAACGGGTCT	TGAAGGGTTT	TTTGCTGAAA	GGANGAACTA	TATCCGGATA	420
ACTGGCGTAN	TACGAAAAGC	CGCACCGATC	GCCTTCCCAA	CAGTTGCGCA	CCKGAATGGC	480
AATGGACCNC	CCTKTTACCG	GSCATTAAACN	CGGGGGTGTN	GGKGTTACCC	CCACGTNACC	540
GCTACCTTGC	CANNSSCCTN	RSGCCGTCTT	TCSTTTCTTC	CTTCCTTCTC	CCMCTTCGCC	600
GGTTCCCNCT	AGCTCTAAAT	CGGGGNNCCC	TTTMGGGTTC	CAATTATTGC	TTACNGSCCC	660
CCACCCCAAA	AAVTNATNG	GGTTAATGTC	CCTTMTTGGG	CNTCCCCCTA	WTNANNNGTTT	720
TCCCCCTTNA	CTTTGRSTCC	CTTCYTTATW	NTGAMNCTNT	TTCCACYGGA	AAAMNCTCCA	780
CCNTTYSSGS	TTTCCTTTGA	WTTATMRGGR	AATTSCAATY	CCGCYTTKGG	TTMAANTTAA	840
CYTATTTCNA	ATTTTCCCGM	TTTTMMNATR	TTNSNCKCGM	KNCTCCNRKA	SSGNTTTCCT	900
CCCCCYTTSS	GKTYCCCCRN	G				921

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

AATTCGGCAC	GAGATANGGG	CGCACCGGGG	TCCGCAGCCG	GCGGGACCGT	CGCCAGCACC	60
ACCGGGGTCA	ACAGCACCAC	GGTGGCGTCC	ANGCAGAGCG	CCGCGGTGAT	GGCGGCCGAG	120
ACGGCRAACA	CCTGCCGTAG	CAGTCGGTGC	GACTCCGCGC	TCGCTCGANC	CATGGCCGCG	180
CCGGCTGCCT	CGAACANGCC	TTCTGCTGCC	ACAGCTTAGC	CAGCANCCAA	ACCGCACCCA	240
GAAACCCACA	CGCCCGCCGC	CCCGGANACC	TGCGCCATCG	KCTGCTGGGG	CGANATCCCC	300
CGATCGCTNA	CANGATGACC	GCTGCCGAA	CGCCCGCGCT	GCCTCCGGGC	AGCCGC3TGG	360
GCSGGGCAAC	CGCGAACCCA	NGAACACGGC	AAGCAGTATC	ANCGCAACAG	CAATTGTCAA	420
GGGCTAAACG	CTTCACATCC	AGGGATCTCG	CGGCGCCACA	CCGTCGGMTC	TGCAGSGCGA	480
CCCCNTCCTN	GGGCGGNAC	TCNTCAAAGA	TGCNGATCNA	CAGKCTAGGT	CTTCGGCCGA	540
TATGSAAGGN	CCCAACGGNT	TTAAAGCGGC	SAAAAAATC	TCCANTGGA	TAAAATCAGC	600
CGGGGANCCC	CCCGTGSCMM	NGTCYCGGKC	ATINTTCAAC	MGGTTTNACG	GCGGKTGCNG	660
GCCAACTKGC	CAAAMTTAAG	KTNGGGGNTY	CGGGGCGGTA	ACCGGCNNTK	NGCCCCTTAA	720
AAAACCGGNC	YTTTCTKGAT	TAMMACCGGN	CCCCCAWTGG	CGGKTGKTCC	CANGNTYAAC	780
AMCCYCCSS	MNGGKTGGS	SAACCCCTCC	CGNGGGGTTC	NTKGTTSCTY	AWMCCCCCGG	840
AAACCSGKYG	GGKTGGCRTN	WASSAMNCCC	CMNGYYTCTT	TAAAGGCCAN	KNRAAWGKYT	900
CCTTGGAAW	CCTNCAATYC	GAAAAYYCTC	CTYMMGSSCN	CTTKCWRTYN	NRNGGGAACS	960
AMWTNYCCNC	GWTTCAWTCG	GGTCCGASMN	AAACKCTTTY	TTTTYCGSSC	STCCMGGSNC	1020
SGGTKNANAN	AAASATTTMC	YYCNNNANKK	YYCSSGCTT	CYKMGRNRNR	GMGAACCCGR	1080
GS						1082

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

AATTGGCACG	AGTGATCGCG	CTGAAGCCGG	TAGCGCGGGT	GGCTCGGGTG	GTTTGCGAAC	60
RAAATCCGCT	CGANGTGGTC	TCGGTAGGCG	GTGTCCANAA	CGGTGGCGCG	GTGCCGGCGG	120
ATCTGATCGG	CGCGGCCGTA	GTGCACGTCG	GCGGGCGTGT	GCAGTCCGAT	GCCGGAATGC	180
TTGTGTTTCG	GGTTGTACCA	GCCGAAGAAC	CGGTTCGAGT	GCACCCGGGC	CGCCTCGATC	240
GACTCGAACC	GTTTCGGGAA	ATCGGGCCGG	TACTTGAAGG	TCTYGAAGT	GGCCTCAGAC	300
AACGGGTTGT	CTTGCTGGTG	TGCGGGCGTG	AGTGCGACTT	GGTGACACCG	AAGTCGGCCA	360
NCANCAATGC	CACCGGTTTG	GAATCATCC	ACAACCCCG	TCCGCGTCMA	GGTCACTTGT	420
NCGGCGCTAA	TTNYTGGGC	GGCAAGGGTT	TGCCGAYCAN	KCCGCTCGGC	CAAAACTTCG	480
ANTCNCSCCA	AGGCCNCCAT	CCNCCCAAAC	AMGTTACGGG	ANAAAAANATY	CAAAGAYCAC	540
CYTCCGGKTN	TTATANCTYC	CCYTTTGSTY	GGGCCCCCN	CYYTGKKNAT	ACCCCTNCCA	600
AWTCCCAACN	CCCKCCAANA	RCYKGGGGCC	CCCNCCAACC	CGGGKGAACA	WTAATTTAAA	660
CCCYAACMAW	ACTWMMNACC	CNNGGGSCCY	AAMCGTYYNR	AGGTTTTTCT	NAAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAASCCK	CCNWTCCCTC	CRASATTGSC	NCCSAAWKSA	780
AKGCCCCCN	TCSGCNWN	CSGCGGKKKT	KKGTTNCCCT	WMRCWMWYTS	GGCCNASCCN	840
CKYYSSMYCC	CCCCCTCCCM	CTCCGNKTCC	CCAMCCYANC	MGGCCCCCYTM	GKCCCCWKNT	900
YKGGCCCCCC	AMMNNNGGGG	WGACCCTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCWGNRA	960
MKCYCCNRAR	ANMCCSCNCC	NGCNCRCNKN				990

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AATTCGGGTG	GCAACGCGGG	CCTGTTCCGGC	AACGGCGCGC	CCGGTGGTGC	CGGTGGGGCT	60
GGTGGTGGCG	CCGGCGGCGC	GGGCGGTAAC	GCGGGGTGGT	TTGGTCATGG	GGGCGCTGGC	120
GGCGTGGGTG	GTGTANGTGC	GGCCGGGGCC	AACGGTGCTA	CGCCCGGTCA	GGATGGGGCG	180
GCTGGTGTGG	CCGGGTCGGA	CRACRCTCGT	GCCGCTCGTG	CCG		223

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

AATTCGGCAC	GANGCGGCAA	CGGTGGCAGC	GGCGGCACGT	CNGTTGCCAC	CGGGGGGGCC	60
GGGAACGGCG	GTGCCGGCGG	CGCCGGCGGC	GGGGCCGGGC	TGATCGGCAA	CGGCSGCAAC	120
GGCGGCAGTG	GCGGAATGGG	CGATGCCCCG	GGCGGCACCG	GCGTCNGCGG	CATCRGTGGG	180
CTGTTGTTGG	GTTTGGACRG	CGCCAACGCC	CCGGCCAGCA	CCAACCCGCT	GCACACCGCG	240

CAGCACAGGC GTTGGCCGCA GTCAACGCGC CCATCCAGGC CGTGACCGGG CGCCCCCTGAT	300
CGGCAACGCG CCAACGGGCG CCCGGGCAAC GGGGCCCCCG GCRGGCACGG CGGGTGGTTG	360
TTGCGCGGCG GAAGGAACGG CGGGTCCGCG GTCANCRGCG GGGCGGGCGG AAATGCCG	418

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCGGCAC GAGGGGCACG ATCGCATACA GCGCTCGCGG CAGACCCGCC CGATACAGCA	60
GCTCGGCACA CGCGAGCGCA CAATACGGCG TCTGGCTGTC CGGCTTGARC ACCACCGCGT	120
TACCGGCCAC CAGCGCGGGC ACCGAGTCCG ACACCGTAAG CGTCATGGGG TAGTTCCACG	180
GCGAGATCAC CCCCACCACG CCCTTCGGTT GATAGCACAC CGTGGTCTTG CCTATCCCGG	240
GCAGCAGCGG CTGTGCCTTA CGGGGCTTCA GCAGGTCCAC ACAGACTCGT GCSTTATAAT	300
TNCGCSTTCC GCGATCAGAT CGACAATTC CTCTTGCGCC GCCCATCGGG CCTTGCCCGC	360
CTCGGCTTGC AGGAAGTCCA TGAAGAACTC GCGGTTCTCG ATNAACAGGT CGCGATAGCG	420
GCSGATGACT GCAGCTCGCT CGATNACGGG ACCTTCGCCA GTCGGTCTGC GCCGCGCGAN	480
CTTCCGCGAA TGCCGCTTCG ACTTCCGCGG NCGTGCCAAC GGAATCNTAT CACGGGTGTC	540
CGGTTAAAC TCCTCAATST NCYGGTCGAA ATTCCGGCAAC TTCTTATCCC GGCAGGTRCC	600
AACSANNCAA ACCTCGGCAA GGTTAGGTT TCCCCNCTT YCAAAAATNC GGKTTTTGGN	660
CMAATTTGCG CKCNATGKTG MCAAGGMTCT CKAANAACGS GGGTCYTCTN NTCNGKGGAK	720
CCAAAMGGKT TTGGGGMAGC GKNMNCCAN CCTWACCCTG KTKAANGGNW TTCCCCCGG	780
GGGAKKNGA ATYCYCCSNA NCCCRGGGG GNMCARATTC TYCCGGMCTC CTCXGGAWTC	840
WGMGTTTTCC CAAAAACSC CCCAAATTMM TTTTTCRCN TRTTGANACW CTTTTKARCA	900
MMCSSAARNS ANMCNCTCYC CKCTKTGKTK AAAAAGNAYW CCCCMAAATT TYTAWTTSSC	960
CCSCGCGGNN CCCNCTNTTT TSCNMTWCTM WNYTNCRMCC MMSNCKSNG KKGGRNCCNN	1020
CRCCSNCCCM AAWYNTKGYN KNTATMAGC	1049

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTCGGCAC GAGGGAATCG AGAATCCCGG AATGGTGAAG CCTCGGTGCC TGCCGTTACG	60
CCAAGAKTCA GGGTGAGCGG CCCCCCGGTG GGAATGCTGA SGCCAACCGG GAAAAGGGTG	120
AGGGCTGGGG TGGAATAACT GAANGTTACT GGGATGGAAA ACCCGGTATT GATATGTATT	180
GGGCCGATCA ANGTTGTGGG AATGGGGGAA GGCTGAGGCG GACCTGTTGG ATTTGGGGAA	240
TTGTYRTGGA CRAKACWGGC CAGCCMCCGT GATGGTTTGG TTSAANTTTT GTGCCGSCCA	300
CANGGTGATG GGATTGATTT TGATGGGGCC SATCGAAATA TTGGGTATGC CNACGCCSAA	360
CGAGATYGCC GGGACSTTCA TGGGCGGGAC AACCMASSGT CCSANGTAAK GGTTTCCTTN	420
ATNTTGATCG GGATTCCGGA ACTMTSTCGA TGSGCTCSAY MTSATSGCCC NACNCCWCCG	480

YTTATTTTMS	GCTNAYGGGA	ATBAMRGAA	CAAYNTCCCT	CCCMGGAAAA	ACCAACMSGC	540
CCTGGTNSYC	CNCCCRCCNC	AKAACCCRTT	KCTGTRSTMC	CCSMAAATNA	CSCCCCCTTS	600
NACTCCNCSG	AANTNSCCCC	CCCSCKNNTT	ATSTYCCCGK	GTTCCCCCMC	CCCTTNAAMC	660
TCCCCCGTTA	ACCCCCWTNT	SNCNCCCCCS	YTAAKMNCRG	GCTTSTTNT	CCCCCYTRMK	720
CNCCCCCTCK	SAMCWNCCNC	CTCKAACNAC	CCCKCYKGS	TNCCCAATNT	WCMWCKCCNS	780
KTNTNMTCK	CCAAAYTNCRC	CCNCRCTCCC	CCKSTSTCAM	WTATAAAACC	WCWYAWYNNK	840
KCNCWMAWTA	MGACWCTCNY	NCCCCNCNCK	NTTKTAMWCC	CKMCCCKCSW	TWCYCKCSCC	900
CCMTCTMNAC	YCCCCCKKTY	NKWMCCCTTC	CCCCCTCCC	MCNMBMKTCT	YCSGKTWCWC	960
NCYNTTMTCN	CYNANMCKCK	KTCTCTTCN	CRNTCTCCC	CCWCCCCCV	KKCTCTSKCC	1020
CNCNCTCCSC	MMKGS					1036

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTCGGCAC	GAGATCATGA	ATAGCGGGCT	GGTCAGCACC	GAAGTGGTCG	GCGATCTCGC	60
GAGCAAGTCT	CGTCTGCTCG	CCCAGCAGGA	GGTCGGCATC	GATGCGGACA	CCTGCGATGT	120
CTTGATGGT	GTTCAAGTGC	AGGTAAGGCC	GACGCCGAG	CTTGCTAGC	AGGGTGCTTT	180
GGCTCTTCGC	ACGTGAGGTA	ACCAATAACT	CCGACGCAGA	CCAACTCCGG	CCCTCGATCC	240
GGGTACCAAG	CTCCGCCGGA	GCCAGCCGTT	GTGCCCCCTG	GGCCGAAGGT	CAGCTGCTGT	300
GCGATCGAAG	TAAGAAACCG	CGCCATGCCC	GTCGCCAAGT	ACGACTGACC	GAGCAAACGA	360
ACGATCGTCG	TCCTTTCCGT	GGGGGTAATC	GANCCAGCA	ACCGCACGAG	CCACCAATCA	420
TTGGGATTCG	GCCACTGACC	GACCAACCGC	CTGTGCGACA	CCCCAGCGGA	ATTGGTGGTC	480
TTCCGCGGGG	CCGCNAACGG	AATCANCSSG	ACGCGCTCGC	CGAASCANCC	GCATANCCNT	540
ACATANCAAC	GGNNTCTGCG	CCCACATTC	GGGTTTMTGC	CCCTCNGCAA	CSSNAAYNCC	600
CCCAATTCTG	AACNAAAAAA	TTGGYCCATY	ARNGTYCTCM	CCAAAAACCN	AWTCCCCCTA	660
TCCCCCGGGG	GGGRCCCCCY	NMNAACCGG	CCCWAAANCC	CCSGGGCSCC	CGGGTTTWTN	720
CCCCCTGTCT	GCCCNCCSGG	TTTGGTCMCM	GGSCMMTNWN	GGGNTGCSCC	CCCNCAAAAA	780
AAAAAYCKNG	NCAAATYAAA	CCCKYCMAAA	ASKTGGS	CCCMARCCGG	GGKAACKWNA	840
ANTTAANCCN	KAAAAAAW	NCANNMCCCC	NGGGNCCTAA	GGKYTTAGGG	GTTSTTNANG	900
ARAAAATMTC	CANATMNSSK	TTNNAAAAAA	ASCCSWAKCC	CCCNNNKKNN	CCAAWKAARR	960
SRCCTTCGGG	TNWNSSGGGG	KKKKKTNCMS	KMNMTTWGR	CCCNCCGCCN	NNTWKCCCTN	1020
TCCNYGGNGC	RNCAGN					1036

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTCGGCAC	GAGTCGATTC	GATCGAACAC	GCCCCGACCT	GGCCAGGCCA	CATGGGCGCG	60
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GCCATGGCCA	ACGCCTACTC	GGCCAACCCG	AATCCATTCC	GCGTCTCACC	GCAACCCCG	120
AAACCGGCGA	CCGCGGCATG	GATCAACCCG	CCCACCCAG	ATCCGAAATA	GCGTCCACAT	180
AATGAGACAC	TGGCGCAAAG	AGCTTGACAG	GCGCCGCACC	ACGCAAGCTG	TTAGACGTGT	240
CGGTCTTGCA	AGAAGCGGGT	TGGCCACCCA	AGATCACGCC	GCCCAAGGGC	ATCGAGTCAA	300
CGTTGCGGTG	GTAACGCGCT	AACGTCGGCG	CCGCCAAGAA	ATGACGGTGC	GCATTACCAT	360
GGCCCTGCTG	ATCACCCTTG	GCCACCTGCG	CACCANAAC	ATGANCAGCC	TTATGCCGAG	420
TCTCGTGGAC	ATCGGCAGCC	GCTTCAAAAA	CTCCTTGTCG	ACAATSGTAT	TGCTGANCCG	480
CCGAATTCTT	NTRCTTGCAA	SAACACTNCA	TGTTNCSGGT	NAACAACCYT	GGTTNGAAAA	540
ACANCCAATA	TTGAANTCCC	ANTCGGGCAG	GAACCNCTM	CGGAAGKTGK	TGGGAACGAA	600
TGKTGCCCCA	AAATCCCGG	NGGTRAAAW	CCCNATG	MSAATTTTSC	CTNGAACAA	660
AAAAGGTCCA	AGKYCAAAG	NGCCCCCCC	SGNAAATTG	TGAACSCAKA	WYANRTTCCC	720
WWWTNCAAT	MTTNGGTCC	KNNTCCCCW	AAANGGSCN	CCCNCCRG	GMGTYTCCC	780
NWNMGGMGN	CYYCSCCCA	AAAAAAMMM	MTTCSGKGG	SMGGKKCCC	CCSGGTWYG	840
GKKYTTAAAC	CCGGKGGTN	CAAAAAANAN	ACCCCCAMS	NGGGGGGAAA	ATTTGNAAWT	900
AAGGKKKTKC	SCMACCCCA	AAANMMNNCN	AWNCCGMGK	SARGGGGRNY	TTMKAGGGMG	960
GNCCCCCW	YCGGGGGNA	NAAYAAAAGK	NGSNGRGAAT	NTTNTTTTGK	RSSSRNKT	1020
TYNTCCTYCN	CCNMGNRWG	SRAMNTGKTS	NSSGGSGGC			1060

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCGGCAC	GAGCTTCACC	AAAGAGCTGA	CATGCCGGGT	GATGCGACAT	CGCATCGAGG	60
GCAATACGGG	CATGGATGAN	CCGAANGGAN	TCTGGCGTTC	GCTCAACTGG	ATTACGGTTC	120
CCAAGGTGAA	ACGCTTTGCG	GCGAAAGATG	CGACGCTTAA	CTTGCGCTTC	CACCGTGCAA	180
TGTTNGTATG	GATGCTGGAA	CCGCGCTGAC	NGATAANGAA	TTGCTGGTTC	GCCGGGCACN	240
ATGGATGGTC	CKSTTTTCNC	TCCGCSGTTA	AATTGCSTGT	GCATCATCTG	GCAGGCTATG	300
TTCCCGCTAC	RCTGCAGCCC	ATCATGGATG	TGCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAMTC	GGGCATSCNC	GCGGCAMTTT	CGCAACCTGC	TGTGTNTGAA	GCGTMTCAAC	420
CGAATGCGGC	GCTYAAAAGC	NGGCTTGCGT	TGATTMMAAC	CNAACCCNTN	CNATYCTTTG	480
CCGNGNMNTG	CGTTCTCTCC	AACTCCGKKG	SYTGCCNCCG	TGAAACCCMA	CTNCCCCCCC	540
GTTGGACTTA	MRTNTTCAAA	AAMCGGMTNA	ACCSGAATNN	SAACCTNCCR	TCAAANTAMM	600
SAANTCGGGC	TTYGGGNRCC	CCCCNGAAYW	TTCKNCNGGG	GMNNTYCTCN	GGTTYNGGCG	660
SAAACNTTTG	CCRTNICYMN	TTTACAMGGC	NCMTNMTTGM	GGGSCSNNAS	GWCCCCGGKK	720
TNTTTNCAAW	TCNCNSKTTT	TTKGGGGGGG	GGCYGRTRMC	NCGGGCCCCC	GGCCCKKMAA	780
AAAAAMCMSA	RRCNCYGGG	KKCCCCCCCM	NNATNGGGCG	YKCRAAACAA	ACCCCAANRA	840
TNGNGMGGGC	SMACCSGNGN	GYNAAAKGGT	TSNSCTMANM	MKGMANNNCT	SGMSCCMNSN	900
NCTGMGGGKT	TTKGNNGARN	AANAMKMGGM	RCGGNCGCNN	GAAAGGGSMS	GSCKSCNNGN	960
NGASNGWMGN	CRNNGANRCC	NCNGYGNMRN	NNGNNNGNNN	GGGRKNVACN	NMKMCAWSMC	1020
NSNMMGNNS	CGYMTNKCGC					1040

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGACAANGG	CGTGAAATGG	GATCCGGCCG	AGCTGGGGCC	CGTCGTCAGC	60
GACCTGTTGG	CCAAGTCGCG	GCCGCCGGTT	CCGGTCTATG	GGGCCTAGTT	ATCTGCGCCG	120
AGCGTGAAC	CAGGGCGAGA	TTTCGGCCGT	TTTCTCGCCC	TGGCTTCACG	TTCCGGCGAAG	180
TKGGGAACGG	TCAGGGTTTC	CAAACCACGA	TCGGGATCGT	GCGGTCGGTC	CAGGACTGGT	240
ANTCCTGATA	CTTKGGTACA	TCGTGACCAA	CTGTGGNCAA	TATTCGGCGC	GCTCCTCGTC	300
NGTCGCGTCC	CGCGCGGTAA	GGTCCANCAC	TTCTTTTTC	TCGTGCCG		348

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGAGACCGG	GTCGTTGACC	AACGGACGCT	TGGGCGCGGG	CCCCTTGCGT	60
GGCATCAGCC	CTTCTCCTTC	TTAGCGCCGT	AACGGCTGCG	TGCCTGTTTG	CGGTTCTTGA	120
CACCTGCGT	ATCCAGCGAA	CCGCGGATGA	TCTTGTAGCG	CACACCAGGC	AGGTCCTTCA	180
CCCGGCCGCC	GCGCACCAGC	ACCATCGAGT	GCTCCTGCAG	GTTGTGGCCC	TCGCCGGGAA	240
TGTACGCCGT	GACCTCGAAC	TGACTCGTCA	CTTCACGCGG	GCAACCTTCC	GAAGCGCCGA	300
GTTCGGCTTC	TTCGGAGTGG	TGGCTCGTGC	CG			332

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	RAGTCGGTCT	AGACGGATTC	AATGCTCCCG	CGAGCACCTC	GCCACTGCAC	60
ACCCTGCAGC	AAAATGTGCT	CAATGTGGTG	AACGAGCCCT	TCCAGACGCT	CACCGGCCCGC	120
CCGCTGATCG	GCAACGGCGC	CAACGGGACT	CCTGGAACCG	GGGCTGACGC	GGGGCCGGCG	180
GGTGGCTGTT	CGGCAACGGC	GGCAACGGCG	GGTCCGGGGC	GAACGGAACC	AACGGCGGGG	240
ACGTGGGGAC	GCGCCCGGCG	GGATTTCTTC	GCACCGGSGC	ACCGCGGGGG	CCGGCGGCGT	300
CGCACAAACG	CACCGCGGGG	GACGCGGCGC	CCGTNGGGCG	GCTTCTKGAT	GGGCTCCGGC	360
GGTNACCGCG	CACGCGGGCG	CCCGGCTCAC	CGCCNGTTGG	GACGCGGGGA	CGCGTNACCC	420
CGATCTTCTT	CCGCNCCCCG	GAAACCGCGG	GGCCGGCCCC	ACATTAKACC	CGGCGGNACC	480
GCGMCCCCGG	CGGAACGGNG	GGYNTTTTCC	AACGGCGGGG	CCGCGGAACC	GNMGGSTGTT	540
CCTTNGGSGA	AGGNCCAAKT	CCCGKCTANC	YYAATCCCCG	ANGGKTGAMC	CTSATGSNCA	600
MYTTMAGGAA	CYTNCCCAANT	KTTSGRACCW	CRCNGGAAA	ASRAWNKNGT	KGGCAAACNA	660

NNTNCYTTKN NATTKGGNNA AAAANCCCTY CCWCSGRAC	NCCCCCNGM GRGMCNNTNN	720
NTTTYGNCNV CCCGGSNAAM RNTTKATTTT NGGGGGNTCN	GGGTKMNNNA AACCCCAAAM	780
MNRNNKCSA ANGGGKSNGC NKNMMNSGT TTTYCKNMRA	MRNWTYKNKN NTCNGARSRN	840
NAAMCNSNK NGKKKNKAA ARNNTTWKTN KNSCNVNCNN	GRRNGVRGGC CKMKGSNMNG	900
MCWHNAWRNG NNGSNCNCKC NNMNAAAAA AASGGVNCKS	NSMKNNKKKG NRGGGGGGGG	960
GG		962

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGCAC RAGAAGACGC CCGAANGTTT GCGCTGGCTC	TACAACTTCA TCAARGCGCA	60
GGGGGAACGC AACTTCGGCA AGATCTACGT TCGCTTCCCC	GAAGCGGTCT CGATGCGCCA	120
GTACCTCGGC GCACCGCACG GCGAGCTGAC CCAGGATCCG	GCCGCGAAAC GGCTTGCGTT	180
GCAGAAGATG TCGTTGAGG TGGCCTGGAG GATTTTGCAN	GCGACGCCNG TGACCGCGAC	240
GGGTTTKGTG TCCGCACTGC TGCTCACCAC CCGCGGCACC	GCGTTGACCT CGACCAGCTG	300
CACCACTCGT GCCGCTCGTG CCG		323

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCGCAGT GTGTGTGGCG GCGTCCAGAA GAAGATGATC	GCGAACATCG CCAGCGCCGG	60
CCAGGCTATG GTGCCGGTGA TGGCCGACCA GCCGATCATC	ACCGGCATAC AGCCGGCCGC	120
CCCACCCAC ACCACGTTCT GTGACGTGCG TCGCTTGAGC	CAAAGCGTGT AGACRAACAC	180
ATAAAACGCG ACGGTGACCA GGGCCAGCAC CCCC GCCAGC	AGGTTCTGTG CGCACCATAG	240
CCAGAAGAAC GAGATCACCG TCNACGTCAC CCGAGTGCCA	ACGCGTTTCG GGTGCGGCACC	300
GCTTCCCGCG CCAAGGGCCG GCGCCGGGTT CGCTTCATCA	CCTTGTCGAT ATCGGCGTGC	360
GCNACCACTT GAGCGTGTG GCGCCGGCGG CSGCCATCAT	CCCGCCGACN ANCGTGTTGA	420
GCATGANCAG CGGATGAATG GCGCCGGCGG TCGTGCCGCT	CGTGCCGAAT TCAACTCCGT	480
CNACAACTTG CGGNCGCACT CGAACCCGGG TGAATGAWTG	AATTTAAACC GSTSAACANT	540
AACTACATAA CCCTTG GGGG CTCTTAACCG GTYYTGAANG	GGTTTTTTGC TTAAAGGAAG	600
AACYATTTCG GGATANCTGG CSTTNWTARC GAAAAGGCC	CRCCCATNGC CCTCCACAGT	660
TTSCCCTGA ATGGSAAATG MNCNCCYKNR CNGGGNCTTT	AACRCGSGCG GGNTTTTGKT	720
MCCCNCTKA CNTTMMTGC ARNNCNGGCC SKCCCTTCCX	TNTYCCCTCC NTCCCCNST	780
TNCNGKTCCC CNNAMNYTNW ACGGGGGGCC YTINGGKCRM	TWTKTTTGG GCCCCMCCCC	840
MAAANASAA GGGGKRNGTY CSTTTGGCNC CCCAMAARGG	NYCCCCCAM YTNRRKMC SY	900
CNNTNKGNN CTGTNCKNCG GAARAMAMCC KCCCCGNSTS	STTNGTYWAG GNRWKGNRSR	960
CCSCCCCGY MNNAAYAWN WMNATNCNNS STNANMAKKN	NNNNNNNSCN WNGNGNNTCN	1020

SCNSNGGKBC CSCC

1034

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCGGCAC	GAGCCACAT	COGGGGCCGC	TCGTTGCATG	ACTCGTTCGT	CATCGTCGAC	60
RAGGCACAGT	CGCTGGAGCG	CAATGTGTTG	CTGACCGTGC	TGTCCCGGTT	GGGGACCGGT	120
TCCCGGGTGG	TGTTGACCCA	CGACATCGCC	CAGCGCGACA	ACCTGCGGGT	CGGCCGCCAC	180
GACGGGTCCG	CGCGGTGATC	GAGAAGCTCA	AAGGTCATCC	GTTGTTGCCC	CACATCACCT	240
TGCTGCGCAG	TGAGCGCTCG	CCGATCGCCG	CGCTGGTCAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCGCGC	TGAGTGCGCC	TCCCGCGAGC	A			331

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTCGGCAC	GAGATCGTCA	CCCTGGCGAC	CAGTGCACCC	AGGCCACGCC	ACCAGTTACG	60
GCTGATGGGC	CAGAAGATGG	ACCAGGTGCT	GCCCATCCCC	CCCACCGCAC	TGCAGCTGAG	120
CACCGGGATC	GCGGTCTCTA	GCTACGGCGA	TRAGCTGGTG	TTCGGCATCA	CCGCTGACTA	180
TGACGCCGCG	TCCGAAATGC	AGCAGCTGGT	CAACGGTATC	GAAGTGGGTG	TGGCGCGTCT	240
GGTGGCGCTC	ANCGACAATT	CCGTGCTGCT	GTTTACAAGG	ATCGGCSTAA	GCGTTCATCC	300
CGCGCACTCC	CCANCGCCGC	GCGGCSGGGG	CGGCCCTCTG	TGCCGACCGC	CCGAGCGCGT	360
CACTGACGCC	ATCTCCGTCG	GCGTTAACCC	CGTGAGAAGG	TGGGTCGTGC	GCAAGTTGGG	420
CCCGGTCACC	ATCNATCCGC	GCCGCCATGA	CGCNGTGCTG	TTCCACACCA	CNTSNGACNC	480
CCCCCAGGAA	CTGGTCCGGC	AMTNCAGGAA	NTYCGTGTGG	GCACCNGCTT	CTTCCGKTRT	540
GGCYTAAACT	TCCNATSTTN	CSGCSGGCCT	CTGGCGTTNC	GNCCGGGCGG	NTCTTNCCAA	600
ATCGGSMMAA	ATCCCCANMC	AAACCCCCCG	GGTCTTGS GG	GCSGGGNGGC	GGCCNAWNCC	660
AAACCCCCCC	NTTAAANTCT	TTGKTNCCNN	CNCSGGCNCC	NCNAANSCAN	CCCTTTKGGC	720
NCTTCCCCCC	CCCAWTTTAA	CCGAKCGSCN	AAYCCCAAGY	TMMGKCCYCY	KNAAAAAANA	780
AATTTGSCSG	CCCCAANTAA	ATTCCCNNGC	CCYTTGGGGG	CGRANCNYNT	TTTMCCSNSS	840
TKGNNAAMC	NGGANCCSGG	KAAYTMMTKG	NAAAYCGCCSN	AAMBNTTTTC	TAANNCCCCN	900
YNCCCSGAAA	ATTNNAMAAM	CMNNKTGSNG	GGGGKTSNC	SGKKGRAGGM	AAAAAANRSN	960
SKTTNMCNNN	SANMNCNSNN	SGGNSNNNNN	NNNCNCGYKC	CSNAANMCCC	CGCGGGGGGG	1020
CCMMCC						1026

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTCGGCAC	GAGAAGACGC	CCGARNGTST	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
NGGGGAACGC	AACTTCGGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGCGTT	180
GCAGAAGATG	TCGTTTCGAGG	TGGCCTGGAN	GATTTTGCAN	GCGACGCCNG	TNACCGCGAC	240
GGGTTTGTG	TCCGCACTGC	TGCTCACCAC	CCGCSGCACC	GCGTTGACGC	TCGACCAGCT	300
GCACCACTCG	TGCCGCTCGT	GCCG				324

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1010 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGCCGC	CGGTGGCGTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTGCGTM	120
ATGCCCAGGT	AGCGGCCCCAG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGCCT	CCAGAGTGGC	CGTGCAATTC	CNGCGTGCTC	CACGGCAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCCC	GCATCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTGNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAATCG	GCGCCGACGG	CGCCCACNAT	AANAACGGGC	ACNACAATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCC	TCNTCCGGCG	NACTTTTCTT	NNAWTAAC TG	CCGCTTCCGK	CCCTGGNGCA	600
WTAAATGGGA	AACCCCTTNC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCG	660
AATTNTTCCG	GANTCGGTGN	KCCGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTYTYYN	AACCSMNAA	MYMTTTYCSG	780
MNAASCCNKT	CCCTTTTAAC	CAMGGSGGTN	AACCGKTMNG	NGGKTAAAAA	GGGSKNNKTG	840
NCCCCYMANG	GGGGGAAAAA	TSTKTCNNCG	GGGCCKAAAW	ACMMMMYGN	GTGKKKNKSS	900
GCSAAATTTT	NMMRAACTKN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKNWNM	SNMNSCSNGG	GKYNSSGSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1010 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCCGGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGCCGC	CGGTGGCGTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTCGCTM	120
ATGCCCAGGT	AGCGGCCAG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGCCCT	CCAGAGTGCC	CGTGCAMTTC	CNCGGTGCTC	CACGGCAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCCC	GCATCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GCGCCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCC	TCNTCCGGCG	NACTTTTCTT	NNAWTAAGT	CCGCTTCCGK	CCCTGGNGCA	600
WTAAATGGGA	AACCTTINCC	CCACCTTGAA	GGGGTTGTG	NATTTTTACT	GSTAACCCCG	660
AATTINTCCG	GANTCGGTCTN	KCCGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTYTYYN	AACCSCMNAA	MYMTTTYCSG	780
MNAASCCNKT	CCCCTTTAAC	CAMGSGGTTN	AACCGKTMNG	NGGKTAAGAA	GGGSKNNKTG	840
NCCCCYMANG	GGGGGAAAA	TSTKTCNNCG	GGGCCKAAAW	ACMMMMYGN	GTGKKKXKSS	900
GCSAAATTTT	NMMRAACTKN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKNWNM	SNMNSCSNGG	GKYNSSGSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

NGNGGGGWNS	NTCAYCAYCA	YCACSGGGYW	CWATTGCGGC	CGCAWCTTGT	MAASAGATCT	60
CGAAYTCGGC	AMGAGGGAMT	CKCTMGCNCC	GCTGTGCAAN	CCAATRAGGC	CTRATAATTY	120
CCACTCCACA	AAAAACCGTT	GTGTGTAYYT	SCCGRAAATR	AAGGCGCCGG	TNTCAACWYC	180
GCCGGTKTTY	CCRATYCCCC	TKTTGTAMCT	GCCKGGGTSR	AAAYCCCCGG	TGTTGGAYCC	240
CCGGATTGAA	ACTGCCGGKT	TGAAACTGCC	GKTTTSGCSA	TCCGGKWATT	GAMSTCRCGG	300
ATTAAAAAAC	CGGKKTGGN	GCTGSNCGTG	CCAAATNCGR	AYCCRATAYC	CCATGGCCTG	360
KYCTYCTCCK	YCGGTACCCA	AAAYCTGGGT	TCCTATACTG	GYCCCTAAAK	GCAAWYCKGG	420
GCTGYCMMTK	TTGCKGSGT	CCNAATTTAS	CACCASCGET	TCCTTCCATA	CCNAAACNCG	480
CKTGGGCWCC	AGMCCGRAAA	AAKAATAAT	RAKAAGGTG	CATNYCCAAA	ACCNCCGCCN	540
CCCNANTNCN	ATCCGNTNCC	MSCNCCCCCA	GCGGTNAAGK	TKSGGAAYTT	CTMMAACCCC	600
CAAANCCCCA	TAACTNCGR	GAASAAACCC	CTYCNCGGGG	GYCNWNCAAA	ACASCNTTAT	660
TTGCTKSTTT	CGGGMWCCGT	GCCGCCNAAA	YCCCCAATA	CTTTYTGGGT	CCNAGAKAAA	720
ACCNCGGGCN	CCMCCCSNAA	NWTATYTCTT	KGGCAANCCC	CSAAACCTTR	TCMNACCNCX	780
ATRMTCCCTT	CCCCVSCAAT	TGGYCGGRAT	NCGSNCCYTY	TCAAARKKSC	CAKWWNNGNG	840
GRRNNACCM	ACCCCAAGTY	CCMNAAAATN	GKCCCCGCTC	CNAACACGNK	TYYTCCSAAA	900
ASCCCWCCCC	CCCCCCCRAA	AACCCCCCNA	RKANTNCCCA	AAAACNYNGK	GGCCCCCCCC	960
CAAACMAAAA	AMCCCCSGM	RMACSGGGGN	NMCCCCGKKK	KKTTTTCTTT	TKCCMRSCCC	1020
AAMGCAMWSY	KSKTNMAAAA	GGAAGRANCN	TYCCSANANM	TCCCNWRSW	CCGSWGMGNA	1080
GAASMCCCCC	CS					1092

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GGGGGGGNNN	NATACATCWT	CYGTGYACCG	GGGMTCTAKT	GGCGGGCCGC	AATCTNGTCA	60
ASAGATCTCT	NAMTTCGGGC	ACAAAACTW	GACAAASYMT	CGNGCNMTCC	GTGTCCTNKA	120
TCGCAAAACG	NGTRACASAC	ASACACRTAT	GTGTGCCCCAC	CASCAAYTCK	TTGGGACCTC	180
GCTRACCGGY	TGCCCCRNACG	CCACGYTGCS	CWTCTATCCC	RACGCCGGCC	ACGGGYGGGG	240
ATATTCCAGG	CACCACGCCC	AGTTTGGTGG	ACAATGCCCT	GGCAKTTTCC	TCRAANTTCG	300
TGAAACCGAA	TTCNSMTTGA	ACCNCCAARG	CCCCSNCCNR	AACARTTGGG	WTCCGCGGTT	360
CTCCCCACCG	KTTTCCGGGG	GTNTCGGCAN	AANCGCACCC	WTGGWTTCTM	TCNCCGCACC	420
GGGCGGACAA	NTCGGGTTGC	AATTTTGCR	AYCGGGGCCG	GGATTCCSCA	AACGGGTGCC	480
GAAACTGTTY	YCRAAMACCG	GGAKCCGCAA	TTTCCGGGCR	ANAAATTTCN	YCNCACTACT	540
GCTTTRTACTT	CCCCGACCGT	AACMANTTTC	ATCGTCNTNN	CCTCTGCCCT	TGGGGCAGGG	600
CKAAAYACCG	CMTTKGGTTF	CGCAACCTGC	GGCCCAANTC	CCNAMCCRCA	CTTTCNATTT	660
GGNTCGAATT	SCCCCCCGGT	RANAACCSCC	NTGGCCNNYT	CGGASSAAAA	NGGGCCCTNT	720
KGGCNSCCCC	AGTAANACCC	TACCNAYTS	CAWTCTTTGC	CAAASTTKGG	ACGAANSKTG	780
GGNTTCCGGK	ATTTYTYTGS	GGNCNCCCTN	TATNGGSNTN	GGGCCCKCYN	NCSTKTGKCA	840
NASSKAYCCS	NGNKGGGGGT	ACCCCCCTMG	GGGGGTTTTT	NSSGCCCCCC	AWAYGNKSTG	900
GCCCCCNNGG	GGAAKAATWT	MWWTMCNSGG	GGGAAWTTTT	NTSTGGAMCS	SGGACYCCCR	960
GGGGGKTTTT	TCCCCCNCSA	NNAWANGGGG	GGGGGANAYT	NTGNSGNGGG	KWNTTTATTT	1020
YTYCYCCTM	TKACMSGGGG	GTTTKAKNG	GGGGGAGAAA	ANAAAAAATA	RAKGGYKNTT	1080
TSKNCACNCT	GKWNWNWANR	NAGAGKTCCT	CKCKCCNCSG	SNTTCTTTTT	MGNSGSYGGG	1140
GNNGNVNAAA	ACNKSRRMAC	KCSYTYCCCG	CGYCTCCTCC	NCNGGGGYGS	NGSCGNSTYN	1200
GNNKGRKWT	TNTMGNCSTN	SCCTCCNCCC	GCKNKNTGTC	TMTCNMYGSG	C	1251

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AAYTCGGCAC	MGAGTATCAC	CAAKCTGYGT	GGCCAGCAA	AGTGGAGCTA	TTACTACCTG	60
TATGTGATCC	TCRACATCTY	CTCCCGCTAC	KTGGTGGGGT	GGATGGTGGC	CTCGCKTGAK	120
TCRAAGGTCT	TGGCCRAACG	GCTGATCGCG	CAAACCTTTG	CGCCAGCAC	ATCAKCGCCG	180
AACAGCTGAC	CTGCMCGCCG	ACCGGGGGYC	GNCAATAACT	CCAAACCGGT	GGCMCTGCTG	240
CTGGCCNACY	CCGTGTCCCA	ANTCGAACTC	ASCCSGCNMA	CCAKMAACKA	NAACCGTTGT	300
CTGAAGCCCA	GTTCAAAAAC	CTCAAGTWCC	GGCCCRACCT	CCCGAAACGG	TNCGAGTCKA	360
TCRSAGGSGG	CCGGGTGCMC	TGCAACCGGT	TCTTCGGNTG	GTRCAMCCCN	AAAMCAAGCA	420
TTCCGGGMC	CGMMTGCCCA	CGCCGCCAAS	TTTCTACGG	GCSGSCCNAT	CAAATTCGCC	480
GGGAACSGSN	CCMCCTCNK	GGAMACGCCC	TWCCAAAACC	CYCGAACGGK	ATCCTTCKGY	540
NAAACNCCGA	RCNCCCKSKT	TCCGGGCTTC	NMSGCGAATA	CCCKNSCMNT	CCGAATCCAA	600
TTCCCMKYGG	CTTTTYYYCC	CCCGGGCCCC	AAAYNGGGYC	CCTASSNMKC	KNCCAMNANT	660

CCNWATCTGG	NGGTCCCNAN	KYYGGCGTTC	NMAATSAMNA	NMNRGGGTYT	TSCYACCMNN	720
AACCGKNNKG	KCCCCMKCTK	MANAAAKATT	RATCAMKWNG	GGNKCKCNCN	NAAMACCSCN	780
CNCYNCWYTC	TMYCSSKWGC	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMCT	CTMTCTCNC	840
MGCGCCKNIN	TYCKSGAKAT	ACASMNKTCC	GCGCNGCGCN	MAAMANRAKA	CTAKCCGYGN	900
CCSNSTMTYN	CTSNNMKMNN	TCCWMWNATC	NTYYGKKCNN	KCTMKATNWC	CSCTSKCNCK	960
MRAMTCKTYG	SNMTCCTCCA	TCNCTCKKSC	SNMSKNTCKC	KSCNCCNCWN	CNKCNMKCWN	1020
GGNSTCRCCY	TCTMNNNTCS	AGCKCGSKNC	WACNCACACK	NGWCTYTTCC	WKNNMKCNKM	1080
TCKCKCACRG	MTMTCWCCS					1099

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GNGNTATACA	TCWCTGTGYA	CCSAGGATCW	ANTGCGGCCG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTGCA	MGAGCGGCAC	AKAKYSTCGT	CCMRACCCGG	CAYACWCCWG	CNCGCCCCWT	120
CTTRGACCGG	GGCKATASMC	ACCGTTGGCC	CCGGCNCGCA	CCTACACCAC	CCACGCCGCC	180
AGCGCCCCCW	TRAMCAAACC	ACCCCGCKTT	TACCGCCCCG	GCCGCCGGGG	CCACCACCAG	240
CCCCACCGGC	ACCACCGGCG	CCGCCGTTGC	CAAAACAGGC	CCGCKTTTGC	CACCRA	296

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

NGNGSGNKM	ATCATCWTTT	TGCACCSNGG	MTCWATTGCG	GCCGCAATCT	TSTMNASAGA	60
TCTCGAAYTC	GGCAMPARCA	TCTGCGCGGN	GAATGTCCAA	AWGTCWKTA	CGGCMATCGG	120
TTTGCCGYCA	ACCACKCTRT	SCAKATGCGG	GCCAMWYCA	AACCRATTAT	TTGGGYCGAG	180
AAAATTTMCG	CKTGTRASCA	ACCTGCAGCG	GGTCAASCAA	CAGCCTCTRA	ACCGTAAATY	240
CKTAGGTNKT	YCCGGCAACA	ASCYCRATAA	TSCGGCCCCG	AMCCACAAAA	CCTGANTNGT	300
TNTTCNCRAA	NCCGGTYCCC	GRAGGGTSA	ACTGCSGTAR	GCTTNTCWYC	NCCTTRACAT	360
TAAACCCCCC	CGGNTCWTCT	CCGCGCCCAA	ATYCYTGCCC	WTKGCNACCA	YCCCANCTTG	420
CSGTATGGTS	RAANCASTSG	GCRAACGTM	MCCSTACCKC	TGGCTGATYC	KTCGGNTCCS	480
SNAATTCGGG	GATTTACGGS	CAMGGTTAAY	CAGGYCCCC	TNTGCTYCKY	CNACAACCSG	540
ATCMWCNCCG	TACCTKTTAA	AATTCTTTGT	GGTGGAACCC	AWYCKAAAAA	NMTNTYCCCN	600
TCCAMMGGGG	CYCGGAAKKT	CNACNTGGKT	NACCCCTNCC	YTTGAASTTT	TCYTGNCCTC	660
GGCCCKAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCTYCN	TGCCCCSTTA	AATTGKNCYC	720
AATCCCKCAA	CGCTCCCCGG	GGTCSGCCMT	TAAAMTTCCC	CCCKSCASNG	GAATYCYKSG	780
GCWGTMATTW	CCNCCCNNTT	CYYGKNAAAC	SCCCCCWKGN	GSCTYCCCN	SNTTSSGCCS	840
GGTTSAMYC	AAAAWTNGGG	MMCNRAGNCG	SGNAMCCSCN	GKKGGSATW	TKAAYCYGG	900
GGGGGTCNYC	CCCCRCSNAA	AAGYGTKGGC	KCCSSSCCYC	CCMARTTTTYT	CNGGMRCMAM	960

ACCANGGGNG	CTCCCGTNCW	WGGCTCCCSN	SNSMAMAAAN	NKCKCCKGGS	CKGARRNMNA	1020
MCTCSNGNGG	WTCCCKXKTC	NSCNSGNCGS	YGGNSASWCC	YNYCNCCACA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

CGCCCCGTTT	TTMMMTTCAY	TCATTCACCG	GGMTCTAGTG	CGGCCGCAAK	CTTGTCACAC	60
GATCTCGAAY	TCGGCAGMAS	ACAATSTCGG	GTKGGGCAAT	GTCNGGTGGG	GCAACTTTGG	120
GCTCGGRAAT	YCGGGGTAA	CGCCGGGTCT	RATGGGTSTG	GGTAATATCG	GGTTTGGTAA	180
TGCCGGCAGC	TACAATTTCT	GTTTGGCAAA	ATATGGGTGT	GGGCAATATN	GGGTTCGCTA	240
ACACCGSCAS	TGGRAATTTC	GGTATTSGGT	NACCGGTRAY	AAYCTGACCG	GGTNCGGTGG	300
TTYCAATACC	GGTAACGGGA	ATGTSGGTTS	YYYACYCCGS	GSAACGGNWW	YTTNGKTCTT	360
TMMCNCTSSM	CKKSAAMTSM	KMGSTSTYCT	MTYCNNGGAS	TAMTYNMCCC	CCGWAYCKSC	420
WAYCCCTCGT	CATYCCMCMC	SGSGYCCTCA	MNCCACCCTG	NGYYCCCTCC	MKMTTCYAYT	480
CMNTCCGGTW	CCTNTMMNCC	CSCNCRYCTC	AMCNCTKSGK	CACCNATMYC	CSACKCHTCT	540
MCYMCSCAKN	MTTCCCTCTN	CCTYTNNCCA	MCMCSTCTTM	TCMAACTCKC	CCGGYCKCNC	600
MYCTCTCKCC	AYNMAACCKK	TYCYWCNWCY	YMYCKCKCAG	WYKNMCTCCW	ACTCTMYNTT	660
TCTCTCNKCC	CMKACCKNTT	CTCWCSCCCC	CCACAKAYMC	YAWCMTMTCC	MCTCKACSCC	720
CYYCNINYCC	NMCWCMTWC	TWNAKCANCN	TTCTTCTCTC	MMYMTMACKC	WCNNTCNCKK	780
SGACCCTCTC	ACTKMKCKCM	TCTCCTTMCK	CCYMWNTTCC	MKYNCCCTCC	NMTCTCKYCT	840
CCTCNCNMRY	CYYYAKCAKC	NMCTCCCCAN	KMCAKCTKCT	CCCCCAKMKC	ACNCKCCCWC	900
CCTCTCTATC	WCTCTCWCTY	ATCTCKCTCW	CNYCMYKMC	ACNCKCYAYT	CNACTMMNWN	960
CCANCNCTCT	CTNYCTCWCK	ACGYCKCKCK	CTMCKCNMYC	NRWCTYRCCT	CKKCCNCCRN	1020
CKNMCMKCTM	CTCTCCWMKM	TCCCWCCCAT	CTMMKSTCTC	WCNMTTCCCT	CNKCCYNYNT	1080
KCYTYCCMYG	CTTCKNTCMT	MCCWCCYATC	TCTMKCCTCT	CWCACYMCAC	WMTTACWNCC	1140
ACTCTCTRCW	CKCKCMCCR	MTCTCB				1166

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

NGNGGNNNNT	CWTACATCWN	TCTNCAACCSG	NGMTCWATTG	CGCGCCGCAW	NCTTGTMNAS	60
AGAATCTCNN	AAYTCGGCAC	ANATGTCTTT	TSIMTAKTGT	GGCGGGGNGC	CACGCCKTAT	120
GTGYGCCTGG	GYTRACCCAA	CCCCGCGGCS	CGGGCCRACC	AGGCGGGGRA	TSCAGGCCGC	180
GGCGGCCCGC	GCGGYTATAT	RAAGCGCCGY	TTTTKTRATA	ACGGTSCCGC	CGCCGGGTRA	240
TTACSGGCAA	AAYCGGKTTT	TTGGGTRTAT	AACGCTAATT	GCAACCAWTT	TTTYCGGGTC	300
AAAAACYCGG	CGWGCANATC	NCGGGYCNCT	RAGGCGCATT	YMCGCCAAAA	WTNTGGGCGC	360
AAAACCCCKT	TSYTATTTTN	TGGGCTATSC	GGYTGTCTTC	GCAAACGCTY	CCCCGGTTAA	420

TCCCKTCCGC	GGCGCCGCCN	AAAAACCACC	AATYCCGYTG	GGGGTGKYCC	CMCAGGCSGT	480
TGCTYCGNGY	CACCTGGCCA	AAYYCCCAWT	AKATTGGGTG	SCYCKTSCGG	TTSYTGCGCY	540
CAATTACCCC	CNCGGGNAAA	GRRAAANA	ATCNTCCNTT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAGGGGC	ATGGCSCGGT	TYTTTACCT	CAAYCCCCNA	NCANTWACCT	YTCCSCCCGG	660
GGGGNCANAA	CGSTTNGCTC	CGSGGNAKCC	TKGTMCCCGN	ATCNAAAGGC	CNGAATTG	720
TYYSSTYCNA	ATTWTWKKKY	CCCCWCNTTG	YAAAAAKCCA	AAASAKCCCK	YCNCAMMYKT	780
NGGGGTYSYG	GCCKNYCTTK	SNMTTAAACC	CYCCCCAAAA	YNSGGGKKT	TCCGCTNSAT	840
KCCACCNCCK	GNGGGGGGNA	SAAAAAAAY	TTTYCCSAAA	ATCCCACCYY	TCYKTKSTRY	900
AMACCCCTT	TYMKKAYTC	CKYSCNATTC	SGMTTCWAAA	TYCCGYGGCT	TNTTCCCCCK	960
CSGGNGCCCC	AAWTTTGKTT	YNCNANTTYC	CCCNAAAMNCM	AWTMGGGGKS	KCCATTCTGG	1020
SCYTMAANTA	AAANAANGGG	NKTTTYCTY	MANAAACACN	GTGKCNCNCN	CNAAMAAASN	1080
AKMAAAKAGN	KKKMTKNNSA	AANCCNCCCC	CTSTYNTYTT	NKTNMNCCKC	CYGGKKNKGM	1140
SWSWYNTTCT	NCCCRCCCCC	YNYNKTGANA	AAMNICYCCS	GGSTMCRNAN	ASNMTTCTCK	1200
STSTNGMGCC	KMBASNANAN	MCAMWKWYCC				1230

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

NGNGGKKNNA	TMAYCWTCTC	ACSSGGTCTA	TGCGGCGCAW	CTMGTMASA	GATCTCNAAY	60
TCGGCANNAN	GCAATMCMC	CATATATAAC	CATTGCGTCS	GYWTGCAWCT	CRAAWCTGTC	120
CTTCSKGCCG	TTKTACRAAG	GTGGMWTGYT	CWYCCCTRAA	SCCCTCRATC	TCKTKTATYC	180
CTKGGGCTYC	ACTTTAACSG	RATKSCTGCC	TTKTAYCATT	RATGCAAWTA	WTGGYCAWT	240
KTTGACAGGC	RACGGCWYCT	TTTYCCGCRA	GRACAATNGA	TTGGAWYCGC	TYCGCRAGGC	300
CCGGCACCAR	ACCGGCNCC	AAAGGYCCGC	GCAAWTSCCT	GGKTCAAAAA	TGGTGCAAAC	360
AAAMCNATCC	CCGGYTTRAC	CGCAGYTAMC	ACAACAAAAT	TCCCWTGGCC	GCACCAWNNT	420
TTYCRATCWY	CWYCCCCACC	TTRAACCTGK	YTGCSGTATT	GCCTKCCTGC	CTCRACAGCM	480
YCNCCCKTCA	AACCTGCGGT	GACTCCAACT	GGTCTGGYCG	AASGGGGGYT	CAMCGGACAA	540
AACCCCRANN	TCGCCAAATT	TTCNCCCCC	CYCGGGAAAN	GKTGATMTTC	TCSNAACCSA	600
CMGGGNNTW	NAACCCTGAA	CSSSGSNKGA	MYNSCCSGGA	ANTTTTCCCT	TYNGGGCGRN	660
AAANCCTTTT	AAGGTACCCC	KGGNGGGGKG	CCCYTTGGG	AAAACAACCC	CKATTGGKTT	720
TGGAAATNTT	TKCNCCCCCA	TTCNSSGGGG	GGGCCCCAMC	CCMMCTTTTN	TCMSCNMTYY	780
YCYYGGAAT	TNYTCGCCSG	GAAYYCGGSM	CCKYCCTAA	NCCCCMNWGG	GKYSTGSNAR	840
GGRATMAWWT	TYSTTTYMC	CCGGCNCNCC	CCCKAKMCNT	KGNTGAACMA	AAAKCSGGGG	900
GSCNMYMWYY	YCINNNGNRTT	TNRGGSSNMT	TYMAAAMMAN	GGGGKYWTYY	CKCCNGSCNN	960
GKTYSGGGST	TTTCCNTTTS	GGGSSATYKG	MACCCCKTMT	AYCCGGGGGT	NTKTKYCCCC	1020
SC						1022

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

NNCGNNKNTA TAMAYCWYCT NCACCSGGGA TCWATTGCGG CCGCAATCTT STMAASAGAT    60
CTCKAAYTCG GCAMGANCCG CAWCTATTTG KGTGRASCGC ACCAGCGRGA CCTCGCSGKT    120
CKTTYCTTGC AGRGAGGCCCK TGGGTGGCRC CGGTGGCAAT GCCAACCGCC CCCCAAAACN    180
CCGCAAATMY CRAAAAACAA CCCSGGGGTA GKTCCSGGCC GCCAAATMAA TAACCGTKTT    240
AACKCAGGCN ACGGCCAACCC GGYCCCGCCC AACCAAGCNA CCTCCCCSCC NATAGGYCCG    300
GTGGGGGCTG CCKTATYKCC AASTCGTCAY CTCNACGGGM CGGYCCMCWT TCCGCCTCAT    360
CCGTCTCTCC TIMMATTTTC CRTCCACYKG GCGGGGAACY TTTTNYCNC CCTTGSCMAN    420
CACCNAAGGY CNAAAATTNC CCMTGCKYKG SNNCAAAYGR GATTGGGGTY CGKKTITTTT    480
TCNMCCMAAC CCCNTTTNA CGCCCMATC CCYTWATACC CCCWWMCMNS ANGKTTGNSA    540
AAKTNCCCCC AAATRCCTAAA MTTCTTCGCC NTTTTMTWMCY YYCCTTTCCC CMCCCNAAA    600
GGSCCRCCYY TCGGGAANTY TCCCNCAAA AWTCAWCCM TTTCCCNCCA AGAAWTTCSG    660
SACTCCTTTN TTCNGGGNAM ATANATYTT YCKTNGGGSK TTCCGMTNC AMMAATNTCC    720
RGGGKAAMCC AGKNTNNTCC YYYCCCCAA NNTYCCYKGG RMCYNNYCY TTAANRASR    780
SAACCCSGG GKYCNCNCSS TARCCCCAM KAAAATTTCC CCCSSKTTT TYNNKQMRW    840
GCCCCCSAAM ACTMTWAYTT TCCCKCGNNN TTTSYCKCS KCAMWMMTG XNCTTTTTT    900
YCSMATAMA CTINGGKCT NTCNYSGCG CMAAANAAGG CGCGSTTCTN TTCWMAMACA    960
YNTSGNMMA SAAKAKWATA AWWNTRKYYK TKNNCCCNCC CKCKCTTSN TNKCCMCSKS   1020
GGGKNWNKKR GWCTCCWCNC CKCCCNCKNK CCKWATMCCC CCCSKCCGM NCMNTTTKT   1080
CCC

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1083

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

GGGGNNKYAT MCAYCWTCTS YACSGGGMNC TATTGCGGCC GCAWYTNMTM GASAGATCTC    60
GAAYTCGGCA MGA AAAAGW GATGTGCTGG ACCTTMCCGC GCGGGACGCR ACCRACAAAG    120
RAASC GCGCC ANAATATTGG CCACAKTTGG TCACATATTT ACCCAATTMT AYCAGGGAYT    180
MCCATTCCCK GGACCRACCG CACAATCCCR ATSKTGGTTT GCRAACCCTR ACCGTCCCCA    240
MYTYCGCCRA STTGAACCAG GGCRAAAAAA CGGCCRAAWY CTCGCCCTGA NTCCCGCTCS    300
GGCNAATAA CTAGGCCCAT TKAACGGAAC CGGNGGCCSC NANTTGGCCA ACAGGTCTCR    360
ACAAAGGGGC CCCASYCGG CCGGTCCCW TTYCACNCCC TNKTCTCKTG CCGAATYCGG    420
WTCCRATNYC CCWTGGGCTT TKTCKYCKYC KYCGGTNCCA AWTCTNGGTA TNCTATRGKG    480
TCCCCTAAAT SCANATCTGG GCKYCCATTT NCTGGSNTTC NATTTAMMAN SRRCGGTTCT    540
TTCWITCCRA AACCGSNTGG GCCCNMCCA AAAAATGATN ATAATAATGK YGSCTTTCAA    600
ACCCCGCCCC CCATTCTRW CSGTTCCANC CCCCNNGGT TAAGKTGGGA ATTTYTNAMC    660
YCNARGCCCT NATTTSGNA AAAACCYCVC GGGYCTCAA CMNYTTTTT GSKSNTCCG    720
GCTCRTTCS CAAAACCCAA ATTNTYNYGG GGYCCKTNA ACMCGGYCRC RCCGGAATT    780
TTTTTGTTT AACCCCAACC TTTTCAASCC NTTTTYTYT TRCCSSCSMN TNGSSGGGNT    840
KSSCNTTCY RARKKCCNMN GGGGGWYCYN CCCCRMNTT CTTTTTTTT CCGTNMMAAM    900
NGKTTCTTCA AASMCCCCC SCCCCNSAA ACCCCCTNAR GTTTTYCMA AANNWYNNGN    960
KNCCCCCCCC MNAAAAAAY YSCCCGNRN ACSMSNGGGA MCCCCCGGSN NTTRKTTTTT   1020
TNCMSGYCCC CSRMASYTT TKAMAMANRR GAMNSMTTTY TNNRGNWKN

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1069

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

NGNGGGGKWK MATAATCWT TCTTCACGSG GGATCWATTG CGGGCCGCAW TCTNGTMCAA      60
SAGATCTCGA TYTCGGGCAM NACCCACCWC TCCRAAAAAA ACCCRAAWCT CGGGSKCTYC      120
GARAAGTGTT GCGCGCKTTR AATTTAACAA ATTCAGTGTC ANAGTGTCAC GGCKTTACWT      180
YCCCGGCAAA GGGGCCACAA CCTGCAGRGA SCACYCRATG GKTGYTGKTS CNCGGGCGGG      240
CCGCKTNAAG GGACCTGCCT GGGTKTGCSC TMCAANATC WYCCGCGGGT YCGCTGGRAT      300
MCNCAGGGGT GTCAAAAAAC CGCAAACAGG CACSCCANCC NTTTACGGGS CTTAAAANGA      360
AAAAGGGCTG ATGCCCCCAA GGGGGCCCGC NCCCAACCTT CCGTTGGTCA ACAACCCGGT      420
CTCTCKTGCC RAATCCGRWT CCRATNYCNC CWTGGCCTTK TCKYCTYCTY CGGTACCCAA      480
ATCTGGGTAT CCTATASTGT CCCCTAAWTT CCAAATCTGG GCTGTCCATT TSCTTGGCNT      540
TCCAAATTTA CCANCAACGG TTTCTTNCAT NCCAAAAACC GNTKGGCKCC NRACCCRAAA      600
AAATGAATAA TAATAANNGG KCNNTTYCNA ACCNCCCCCC CCCNATTCCA TYSNGTTCCA      660
NMNCCCCCAG NGGKTAGGK GGGAAANYC TCMACCYYCA ANCCCTWARS TTTTNGRAAT      720
KAAACCCTYC YCNGGGTCW TYMAAAAAMA NTTATTTGGN NGNTTTCGGG MWNCKRKNST      780
SCCAAAATCC MAAATANTTT YTTGGTYCNA TWAAAAAMCG YGNCCMNCCC GGAAAAWTTT      840
TTNTGKTTSA ACCCCAAAAC YTTTTCMNAA NCSSKTTTTY CYTTCCCCC AMNWTGGGYS      900
GGGNATKGYG SCYTNTCTTA TKTKYTYMTW CMGGGGGGNN MKMTCMMCCC CCMTTTYCY      960
NYWRTTTTTN KCCCCKTNMR NNRAANNNGN YTCSYNANAA AAGCNCCCCC SCCKNCCCN      1020
AAAAWCCCN NMNARAKTNT TTMKANRMN SCKCNKNGKY YCCCCCCCWC YNMNNAAAAA      1080
AATMYCCNCC RASANMCASM NMGGRGNRSC CCCCCCSTT NNNNTMTTNT TTTTTCSRA      1140
GAGCKCCSCG MNANMKNCK CTTTTTKCNC NNGNNGNGNN GNGMNMCKCC CCNAGAAMWK      1200
CTKSTCCCKS                                     1210

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(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

NGSSSNGMNA TMCATCWYCT GYACSGGGMT CWATTGCGGC CGCAACTNGT MAASAGATCT      60
CGAAYTCGGC AAKANACACC ACCGCCGTGT MTATACACCG CAAATGTTCT GKTGTCCAAA      120
ACCGAGACGC GCGGCGCGG GGGYTCCAAC GCKTTACYTR ACCCGCCAGY TCAGTGTTTRA      180
AACCGGTGYT RAGGGCCGCA CCCAACWTAA ACGCTTTAKC CAAGRAWYTG GKTGGCCCCG      240
AGCCACCTGY TGTGGYTGCC CTCWYCGGTG GTAGCGCCGG TTANCGCCGG TTGCGCGYTC      300
AMCASCSCGC CGGTRATCCC AKCNWTCGCC CGGCCMRACC CACCGGGCAC TTTGRACGGT      360
GCGGCCAATT CAAAYCKYCT GRWTCCTTCM AAACACCACR AAGGCCACCM CCMSCACCNA      420
ATMGGGRACT TTAAGGCCCA GGCAAAACCT NTRAKNCCT CCCGGGCRAA GGTCCSGCAA      480
SCRATCCMAA AAAAKCKNAT TTCCCCCAGC AKCAACCCAA MMCGSTTTGC TGCTTCCGGA      540
TTGGAAMCCA ATTCWGGKT NCNWGGGAAA AACASCNNCC NWTAKCCMGG CCCMCGGGCA      600

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ATTTCSGRAA	SAACCCCTNY	CCCGGGTTTT	YCCTGCTCMG	GCCCAANACC	CCCGGGAATC	660
AAAAASGTC	GGNCAAANGG	GCMAAACCCS	SACCCMACTT	WTTCCRCTTN	GGGGGGSCWN	720
CCKNGTTTAA	AWKSCCTCY	CTSCCCAAAY	TCGGKCMAAA	NNGRKTTGGK	TTNGGCNACC	780
NTTTCGGKGC	CCGGGKGGK	WGKYCTMNMA	CSTTTINTTTT	SCCCCYKAAA	NYSCCCCCC	840
CGGSSCCCCG	CCCGGGGGGA	NNTTTTTTAMA	GKKTYCCCCCT	CCCCAMAAAA	ANACCCCN	900
CCSGGSCCCT	TTKRWAAAMN	KCTSCCCCN	GNNGGGGKCM	GGKTTATTMT	NNNCCSCC	960
TCCGCGSAAA	AAATAKMTT	SYCCCCCNC	CTCCKNCKNR	GKAMSMSCGC	TCCCYCTCNC	1020
GCNKNTWAAN	ARSNCCKKN	CCNCYKCCGS	NSNGKCNWCD	NCCSTSSNCT	NKGCNCKN	1080
KAAANAAYNC	NGSMSTSSMN	CNKCC				1105

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NGSNSNKNNN	TAMAYCWYYC	TSCACSNNGA	ACWANTGCCG	CCRMWCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCGGC	AAGAGTGTGT	GCATCTGGTC	ANAGTSTMTA	CRCGGTGCCG	120
CSGGTGKGR	GASCACMCAT	NTGCGRACAC	CAAACCCCTC	GCGGGYCACC	GGCKTCGCCT	180
GCAAAYCCT	CCAGGCCACC	TCRAACAAYW	YCTYCTGCAA	CGCARGCCGT	TYCGCGGCCG	240
RATCCTGGKT	CASYCAGCC	TGCGGTGCC	AAGKTACTGG	CSCAYCAAAA	CCGCTCCGGG	300
RAACRAACKT	AAWTYTGCC	AATTTCTTTC	CCCTGCGCCT	TGATAAATTT	NTNAAGCCAC	360
CGCAAMCCTY	CGGGCKTCTC	CTCKTGCCRA	ATYCGRWTCC	RATAYCGCCA	TGGCCTNKTC	420
KYCTYCKYCS	GTACCCAAAT	CTTGCGTATC	CTATANTKYC	CCWAAANRCA	AWTCTGGGCK	480
KTCCATKTSC	TGSKTCCRA	ATTTAMMACA	NCGGTTTCTT	TCWTACCAAA	AACCSNTGGG	540
CCCCRACCRA	AAAAGGATAA	TAATAAKGTG	CWWWCAAAAC	CCCCCCCCC	RRTTCAAYCG	600
GTCCARCACC	CCANGNGGTN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	SNTTNSGNAA	660
AAACCCCCCN	GGGYMYCAAA	AMMCTTTTTG	GGGMTTCSGS	CCATKGYKCC	AAAACCAAAA	720
TMTTTCYGGT	CRWAAAAACC	GGCCCNCCCG	NAAATTTTTT	GKCAACCCCA	AACCTTTMAM	780
CCNNNTTCYY	YCCNSACAA	TNGSGGNKN	NGSSCNTTYT	TWTTTYYNNA	GGGGGGRRWC	840
SNCCCCNAAN	YCCNAANKG	NKCCCGSNMA	AAAGAGANTT	YCMKAAAAAC	CCCCNCNCCC	900
NAAAYACCCC	MAAAKWTCM	AAASMSCNNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

NNNGNKNNNY	ATMMAYTCWY	YCTSCACCSG	GGNNWCWATT	GCGGCCRMW	KCTTGTMAAS	60
AGATCTMNAA	YTCGGCACAG	ASSSGCACAG	ASC CGCGCG	CTATYCMYCC	GYTGCTCATG	120
CTCAACACGC	TCKTCGGCGW	GRATAATGGC	NCGCCGCCGG	CGCCAACACG	YTCAAYTGCT	180
TGCGCAACGC	CATATNTCAA	CAAGGTRATA	AAASCAAAAC	CGCSCGCCGY	GCCCTTGGGC	240

SCGGRAASCG	GTGCCAACCC	RAAACNCKTT	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TCKTCCTCCT	GGGCTATGGT	GCGCCACAAA	CCTSYTGCG	WGGGTCTGGC	CCTGGGYCAC	360
CGYCRNNTTT	TATNTNTCK	YCTACACNCT	TKGGTYCAAC	CAACCCACTT	CACMAAATTG	420
TTTTGGGKTG	GGGSSGCCG	YTGTNNCCGK	TAATAATCSG	NTGKTCGGCC	MYCACCGGWA	480
CCATANCCTG	GCCGGCSCTG	GCAAAATTCC	SAAATCATYT	CCTTCTGRAC	CCCCACAMRC	540
CTNSAAATCC	GRATCAATNC	CCCNKGGCTT	NTCYCTCTCN	GTRCCCAATY	TGGTTTCTAT	600
RKTNCCCYAA	TSCAATTGGS	TTYCCRTTSC	YGSTTCCAAN	TTNACAAMAS	GGTTTTTCMT	660
ACCAAAACCC	NTGGSCCNNA	CMNAAAANKA	RAAAANAKGG	KCTTTYAAAC	CCCCCCTAT	720
TCAWYCGGTN	CMRNWCCCCG	NGKAAGGKGN	GAAAYTTTHA	CCCAANCCMT	ARSTTSGNAK	780
AAACCCYYCG	GGGTSMCAAA	MKNTWTTSSC	CTTCGGMCTT	YCCAAATMSA	AAATYYTCKK	840
KRMNAAAAMC	YGNCCCCSAA	ANATTTTTGT	NAAMCCCKMA	YYTRTTWMCC	WTTTTCCYCC	900
CCMCNNSNSG	GNTNCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMNTYTT	TWTTCKWCWN	960
MMARGSNNTY	RGRMMNMNCC	CCNCCCCNAK	MTCCNCAAAK	NTTTNAACNN	NNKYCKCCCC	1020
CCCMWMNKNC	CCCMNCMTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

NNSGSGMKKK	ATAMATCWCT	CTSYACCSNG	GMTCWATTGC	GGCCGMAWTC	TNGTMAASAG	60
ATCTCGAAYT	CGGCAAANAK	ACGCMAYGTC	AAGTGTRAYY	CGGTCACATA	TCMTGCGNG	120
TCAACMCCAA	AGCCGNGTCA	CCGYCTCCCT	GGGGCGCCAC	CCCCATCGGT	RATGCAACYT	180
CGCGCGCCAC	CGYCAAAAGG	KTCWTTRAGG	CGCTAAAGGT	CAMCAATTCC	TRAGGTMCN	240
CACCGTTNTT	TGGCCCCGCC	RAWTYCTRAC	CCGCAATWTC	GGTAATCGGR	AATTTGGGCW	300
YCGGCTTGGG	CAATAAGKTN	TTGGGCAACG	GCGGRWTCYC	NCTGGCCGRA	ATTCCNCAT	360
TCKXTTAAAG	GKTGRACCGT	TTYCCCCGYT	GCCGTAAATG	YTYCNTGGGC	GCCYTCGGCC	420
CRNAGCASY	CRCTAACGGY	CMCCAGGCAA	TACCKTTGGC	TTTRAACCAC	CGGRATNAAY	480
TGKTACCCAC	YTCAASSGTS	CTGRANTTRK	TNCTNTGRAA	AANMCCACCN	AACCCGGNTT	540
RATCTGCTTC	MTCANCWTTT	SCCGGGTTCT	GCCGTTTTGR	AACTTNATC	CMTYCAAAAG	600
GTTTTAMTTT	CCAANRAATT	CGGYTTGCCA	CCTTGGCCGS	GGCTGGTTTM	CGMWCCTTTR	660
AMATCCNCCS	GCGGGSAAAN	AMTTSGGNTT	SGSCCGGTCC	CCCGNAATAT	YCNTGGNCCT	720
GNAAATTGSS	GGGATCCCCN	GSGNAYCCGG	CCWTKGGGGK	TNCCCAGTTG	GWACAATTVC	780
WKCCGTTCCA	AACCCGGGNC	CGGGGGGTGG	GSCCCTTTTT	CCTMYNNAAA	AAGKGTITGN	840
NYTTTTTCCG	CNRAANTTCA	CCSKCNKTNT	GGNCCNAACY	YYYCAANTTC	CANACCTTTA	900
AASAAANCYK	YGKTYCCCCC	TTTTMCCSGS	SANCCCCCM	NMSSKNCGGG	AAAAAAGNK	960
TYNGCCTTAN	CNSNKTKTNT	TNKTYCCCCC	NMWNNSNMCM	NCBKCKNKRY	NGNSNMNCCT	1020
MKYSKCNWNN	SNNNNNKCNG	GSNCSGMKYM	CMNNCNGMYK	NGNKSNNCCC	MSC	1073

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GNSNGNKNTN	TMCAIYCWYCT	SCACSGGGTC	TATTGCGGCC	GCAATYTNGT	CKASAGATCT	60
CGATYTCGGC	AMNANAARTG	TCGTCGTCAA	TTTCAGKKTG	GTCKTCAAAY	GGGCCAGGCC	120
GNACCRACA	CCCTGNGTCA	CCCCAAANAC	CAACAGCWTC	AAATWTCAAG	GCCRAGGCSC	180
TRTCAATYCC	CRASAKTTA	ACCGTKTCW	TCRAAGGTGC	CRAACCAGGC	ACCCAGYTCA	240
CCGCCSGGCA	AWTCGCGCTG	CCGGCCGGTN	TCAGCCTGAT	TYCTGACCCT	RWTCTGTSGG	300
TGGYCAMCNT	GGTGAAGGCC	CWWCCGCCNA	AGAACTGGAG	GGCRAATTCC	CAGGANCCNA	360
GRAACCCNAG	GAACCCGCGG	TAKAANCCGG	CRAAACCRAG	GCCGYTGCCN	ATTCCNATTA	420
NAMSGGTTTG	CRACNTGGCC	RAACCGTTTY	CTTGGTCGGC	CTCGGCAACC	CTGGACCANT	480
TACCCCKTNC	CCGGNMCMAC	CYCGGGTNCT	TGKYCCCAAT	NTGCTCCCGC	GNRANTNGGC	540
CNAATTCCAG	GGCNCCANCT	TTCCGGCCCN	AATTCCTCTG	GTAAATCACC	GGGCNCNCCT	600
GGTTTTGGGC	AACCCNCYS	CTTMTTTAAA	CATTCCGSCC	CAAATGGGNC	STTGGSAAT	660
TCTNTYCGGT	GGGGCSGGCR	ANMYTTCTCT	YCCNAASAN	CTTAMYCCAN	TTCGSSNTCC	720
CGGKCAAAWS	NGGGGGGGNA	AAGGGCCCCC	CGGNTSCKCC	GGGGKKGCCC	CYGGKTTCAA	780
AANTTTCSGG	GKTSTMSCGG	NVTCSCCCCC	CSGCCAAGRA	CCGNGGTTTT	TTTTTGAACC	840
KCMANTCSSA	AMCCGCCSSC	CCCMAAAGGS	GCCTNAAWGR	RAYTTNKSCC	CNNAAACSGG	900
CCCCCAKYTY	SGGKTTTCNN	CNCCSGKKG	CCMTSTTTMM	MRCCCTTTGN	GNKTTTTTAN	960
MGSCCTTNNC	CACCCCYCK	GGGKCSMNNA	GAAKTMYWKC	CNGGGGNAN	RSCCCCCNCN	1020
GSKGGGGGKG	MGAGYSCKT	CTKGCNCNN	YKNTTTCCTC	C		1061

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GNNGNNNKWN	ATMCAIYWY	CTSCACCSGG	GMTCWATTGC	GGCCGCAWKY	TNGTMAASAG	60
ATCTMGAAYT	CGGCACANAG	CGGCACAGAG	TGTGTGCATC	TGTGTGANAG	CTGTCAACGC	120
GGTGCCGCSG	GTGGTRASCA	CMCATTGCGR	AACACCAAAC	CCGTCCGCGG	GYCACCGGCK	180
TCGCCTGCAA	AAYCCTCCAG	GCCACCYCRA	AACAAYWYCT	CCTGCAACSC	ARSCCGTTYC	240
GCGGCCGRAT	CCTGGKYCAS	YTCGCCKTGC	GGTGCGCCAA	GGTACTGGCS	CWYCRANACC	300
GCTYCGGGRA	ACCNAACGTA	AATCTTGCCN	AATTTGCNTT	CCCCCTSCCC	TTRATNAATT	360
TGTTAAACCA	CGCAAACCTY	CGGGCKTCTC	CTCKTGCCRA	WTCCGRWTCC	RATNYCGCCA	420
TGGCCTNKTC	KYCTYCKYCS	GTMCCCAAAT	CTTGGTATCC	TATATTGTCC	CTAAATGCAA	480
ATCTKGGCTG	TCCATNTGCT	GGCGTTCAA	TTWAMANCAG	NGGTTTCTTY	CTTCCNAAAC	540
CCSTTGGCCC	CAAACCNAAA	AATGATNATA	ATAATGGTGC	TNTCAAACCC	CGCNCCTATY	600
CNATCSGKCC	AMMCCCCRGN	GGKTANKKGG	GNAATTCTMM	AACCCCAAGC	CATAASNTTG	660
SGANAAACCY	NCNCMGGYCA	CCAAAACANY	NTTNTTGGNY	SSNTTCGGMN	YCATGGCTNN	720
CMAAAACCCA	AATACTNYYG	GGYCCAATAA	AAMMSGGY	SAMCCGGAAA	WTTTTTYTGN	780
KYNAACCNAA	AAKCTTTTTT	CNAACCCDAN	WNTYCCTNCC	RCRCMANTGG	CNSGGARTKT	840
SSSCTTNCCA	ATGKYCCMAA	AGNGGGRANA	CCARCCCCAA	TTCTTNNTN	KNKNCCCNST	900
TRNAAAAGGG	GKNTYNCMAA	AASCNCCNCC	NCNCTCCCAA	AAKAMCCCCN	AAAGAKNTCN	960
NAANASKYSN	NNNSCCCCCC	CCMMMN				986

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGNGGGNKRN	ATMMAYCWCT	SATYYACCSN	GGMNMWATTG	CGGCCRMWAT	CTNGTMKASA	60
GATCTMGAAA	YTCGGCAAAG	AGYATKCTCG	GGGGCCAGAT	TTNTGGCCCG	CAACCGCCGC	120
ACTTTGCAYW	TCAACAKTCC	SGGTGCCCCA	AAAAAWTCWT	ACCCCATMC	TYCKTGCA SM	180
ASYTGCGCCC	RATTRAACAC	CCGGCCGGCW	TGCTGCGCCA	GGTATTYCAS	CAGYTCAAAY	240
YCTTTKTAGK	TAAAATCCAG	CSGGCGGCCA	CNCAGCCGGG	CGGKTAGGT	GCCTYCRCA	300
ATMACCAGCY	CGCCCAGGGY	CACCTTGCCC	AAAAYCTCCT	GGGTCAGCCA	AATTYCCGCS	360
CCGGCCAACM	ACCANCCGCA	TYCTGGCNTC	AATCYCACCG	GGCCCCGGTGY	TAAAMMANMA	420
GRATCTCXTC	MANCCCCCAN	TCAGCSYTNA	CNGCMACAGC	CCGCCTTCTT	CAMACCGCCA	480
RTACCGGGWT	CAACCGGCCS	GTCAAACCTCA	ACAGGCGGNC	AGGCCTCCCC	CGGANSAAAG	540
GTCTTACSCC	NNYAANAAAA	MAAGNTCTGT	TTTCCCCCTC	CASAASNAAA	AANCCCCSGC	600
CGGGCCTTCN	NMMGGGTTTG	GGGMANANAA	AARCNCCGGN	GGAACGNATC	CGAAAMCTCC	660
CAAGTCNCMT	TWAWAACYCN	NNAACCCCCC	ANTTTTGGGA	AAGGNTCCCC	NTTMYCCCCC	720
TTTTASGKTS	GGGMMYCTY	TAAAAAAATT	CCCCAAAAAG	CCCCGGGAAG	GGTCMAMCTG	780
GGNAAATTTT	CAAMCCNWGK	TTNTTYNGGT	TMCGGGGGRA	AATTYCNCCT	CCYNNNGGG	840
CSSGSNNNAT	TAYGGSNMT	TTTNNAAWTM	NSGKKT SAMM	YNNKCCMNNN	SNNMSMANNK	900
TNAMKCCCN	CCTCNGNGKY	CSCYNCCCSG	GNAGNGGRAS	MKCCNANMAA	AYASGNTTNK	960
CGGAAMMCNN	AATKGNNSC	CCGGASMCNN	NNNMAAATMT	CNCNKCSNN	AANRGMRA CN	1020
CCCNNSGMMN	RRGAARM TNY	YCCCCGSKM	GKGNKAAAAW	GKYCCCCCM	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NGNGNCNKNT	MTACATCWTT	CTGCACCSGG	GNTCWANTGC	GGCCGCWKY	TTGTGASAG	60
ATCTCGAAYT	CGGCAMGAGG	ACWCTCGCRA	CGCCCCCACA	NACTCTGGCG	TGTGTACCCC	120
ATTGNGCGCX	TCACGCGCCC	AYTGANCCAK	TNCACTGGGG	TGCCGTYCGC	CKTGCGCGGC	180
GGCCTCACGG	CKCTSCWTCT	RAAGGCWTGG	CGCACCGCAT	TCGGTTTTCT	RAACGCTGGG	240
AAAWTGGCCA	GCCGTCTGGC	TCATGGGNTC	TACGCAACGC	CNGCCCCCAA	CRCTTTCTTA	300
AATCCGGYCC	NTCCTGANCS	CTTTGAAYCC	CGGGGSAAGA	ACTGGTTGCS	CNCGAYCTGC	360
TCGAACTTRK	TCNAAATCCC	GCANAKTGTT	TCNTAMGYCC	CNCCGGAAGG	NGAACCTACT	420
TTCNGGWANG	TCGGCNKCCG	GCGCTTATCA	STCCTGATCA	ACGGGGA ACT	GGYKNNSTTG	480
KGGGAAAAAG	RRCCTCAATG	MTYGGTCCCK	GCTGCGKANC	CGCSCCCTGK	GYCGCNAATG	540
GAAGGCSMAG	GGTTAANGCC	MTTYCNYCCR	RSCCGTSTGA	SGKWTTYCGG	MGGANKAMNN	600
NNKMAMWTTK	TCRNGGGCCW	ATSTSCGGG	CKSTTAKAGA	ANACTYCKKW	WCCGTNTYSC	660
SAAAGNTKCS	GCGMGTTTTTS	SCCKMGANGN	YCTGATTTSA	GGGGGKYKCC	CCCGGGGTYC	720
CGAAWKWRKY	CCYAGGGGGM	GNYSAGCSC	CGMNNATNAG	AGNAAGGKTT	RYGSTSKNCC	780
TYTNKGGACC	WSCNNCWSAK	ANAAACNNKKT	TGCSCCNTMS	AGNKTNKGRT	YCCNKSTTTC	840
TAAGAGGAGC	TATKMKCGCC	CKTGGANGMM	GAGWGMGCCG	KYCCCSNKRT	TCNTNGWAAA	900

TATKSAGMGG	TKCCGMAGMK	CCSCGTTTKT	TKTGANAAMN	MSMRKNKKTG	CGMGYTCTSC	960
GGGNTTTGTA	GAGTAKTCGS	CSCSSMWGAC	WCSGMCNGNG	AGKNKTNNTS	YANTGARCGY	1020
MNNSKTMKMT	MSCSCGCGNA	GGAGNGCCCC	CSANGMSTGY	NKGGNMSSNG	ARAKGATGGS	1080
GGCCNCGMNN	MGMGGANMGA	SANNGMGMGR	GGGGGKTGKC	TCKCSCCGNS	CSANGRAGAA	1140
GKTCNGSCGC	CGMGGKYGKT	KTKTKNKTGG	YSTCMSSMMM	NAGAAAAGAG	AGGGC	1195

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

CCATCTGATC	GTTGGCAACC	AGCATCGCAG	TGGGAACGAT	GCCCTCATTC	AGCATTGCA	60
TGGTTTGTG	AAAACCGGAC	ATGGCACTCC	AGTCGCTTC	CCGTTCCGCT	ATCGGCTGAA	120
TTTGATTGCG	AGTGAGATAT	TTATGCCAGC	CAGCCAGACG	CAGACGCGCC	GAGACAGAAC	180
TTAATGGGCC	CGCTAACAGC	GCGATTGCT	GGTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGCGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGGTCAGAGA	300
CATCAAGAAA	TAACGCCGGA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATG	GCATCCTGGT	360
CATCCAGCGG	ATAGTTAATG	ATCAGCCAC	TGACGCGTTG	CGCGAGAAGA	TTGTGCACCG	420
CCGCTTTACA	GGCTTCGACG	CCGCTTCGTT	CTACCATCGA	CACCACCACG	CTGGCACCCA	480
GTTGATCGGC	GCGAGATTTA	ATCGCCCGCA	CAATTGCGGA	CGGCGCGTGC	AGGGCCAGAC	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTTGCCCGC	CAGTTGTTGT	GCCACGCGGT	600
TGGGAATGTA	ATTGAGCTCC	GCCATCGCCG	CTTCCACTTT	TTCCCGCGTT	TTCCGAGAAA	660
CGTGGCTGGC	CTGGTTCACC	ACGCGGGAAA	CGGTCTGATA	AGAGACACCG	GCATACTCTG	720
CGACATCGTA	TAACGTTACT	GGTTTCACAT	TCACCACCC	GAATTGACTC	TCTTCCGGGC	780
GCTATCATGC	CATACCGCGA	AAGGTTTTGC	GCCATTGCGT	GGTGTCCGGG	ATCTCGACGC	840
TCTCCCTTAT	GCGACTCCTG	CATTAGGAAG	CAGCCAGTA	GTAGGTTGAG	GCCGTTGAGC	900
ACCGCCGCGC	CAAGGAATGG	TGCATGCAAG	GAGATGGCGC	CCAACAGTCC	CCCGGCCACG	960
GGGCCTGCCA	CCATACCCAC	GCCGAAACAA	GCGCTCATGA	GCCCGAAGTG	GCGAGCCCGA	1020
TCTTCCCAT	CGGTGATGTC	GGCGATATAG	GCGCCAGCAA	CCGCACCTGT	GGCGCCGGTG	1080
ATGCCGGCCA	CGATGCGTCC	GGCGTAGAGG	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	1140
GACTCACTAT	AGGGGAATTG	TGAGCGGATA	ACAATTCCCC	TCTAGAAATA	ATTTTGTTTA	1200
ACTTTAAGAA	GGAGATATAC	ATATGGGCCA	TCATCATCAT	CATCACGTGA	TCGACATCAT	1260
CGGGACCAGC	CCCACATCCT	GGGAACAGGC	GGCGGCGGAG	GCGGTCCAGC	GGGCGCGGGA	1320
TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	CATTGAGCAG	GACATGGCCG	TGGACAGCGC	1380
CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	AGTGTCGTTT	AAGATGAGGC	CGGCGCAACC	1440
GAGGGGCTCG	AAACCACCGA	GCGGTTGCGC	TGAAACGGGC	GCCGGCGCCG	GTAATGTCGC	1500
GACTACCCCC	GCGTCGTGCG	CGGTGACGTT	GGCGGAGACC	GGTAGCACGC	TGCTCTACCC	1560
GCTGTTCAAC	CTGTGGGGTC	CGGCCTTTCA	CGAGAGGTAT	CCGAACGTCA	CGATCACC	1620
TCAGGGCACC	GGTTCTGCTG	CCGGGATCGC	GCAGGCGCCG	GCCGGGACGG	TCAACATTGG	1680
GGCCTCCGAC	GCCTATCTGT	CGGAAGGTGA	TATGGCCGCG	CACAAGGGGC	TGATGAACAT	1740
CGCGCTAGCC	ATCTCCGCTC	AGCAGGTCAA	CTACAACCTG	CCCGGAGTGA	GCGAGCACCT	1800
CAAGCTGAAC	GGAAAAGTCC	TGGCGGCCAT	GTACCAGGGC	ACCATCAAAA	CCTGGGACGA	1860
CCCGCAGATC	GCTGCGCTCA	ACCCCGGCGT	GAACCTGCCC	GGCACCGCGG	TAGTTCGCT	1920
GCACCGCTCC	GACGGGTCCG	GTGACACCTT	CTTGTTTACC	CAGTACCTGT	CCAAGCAAGA	1980
TCCCGAGGGC	TGGGGCAAGT	CGCCCGGCTT	CGGCACCACC	GTCGACTTCC	CGGCGGTGCC	2040
GGGTGCGCTG	GGTGAGAACG	GCAACGGCGG	CATGGTGACC	GGTTGCGCCG	AGACACCGGG	2100
CTGCGTGCCG	TATATCGGCA	TCAGCTTCCT	CGACCAGGCC	AGTCAACGGG	GACTCGGCGA	2160
GGCCCAACTA	GGCAATAGCT	CTGGCAATTT	CTTGTTGCCC	GACGCGCAAA	GCATTGAGGC	2220

CGCGGCGGCT	GGCTTCGCAT	CGAAAACCCC	GGCGAACCAG	GCGATTTCGA	TGATCGACGG	2280
GCCCCCCCCG	GACGGCTACC	CGATCATCAA	CTACGAGTAC	GCCATCGTCA	ACAACCGGCA	2340
AAAGGACGCC	GCCACCGCGC	AGACCTTGCA	GGCATTTCTG	CACTGGGCGA	TCACCGACGG	2400
CAACAAGGCC	TCGTTCTCTG	ACCAGGTTCA	TTTCCAGCCG	CTGCCGCCCC	CGGTGGTGAA	2460
GTTGTCTGAC	GCGTTGATCG	CGACGATTTC	CAGCGCTGAG	ATGAAGACCG	ATGCCGCTAC	2520
CCTCGCGCAG	GAGGCAGGTA	ATTTGAGCGG	GATCTCCGGC	GACCTGAAAA	CCCAGATCGA	2580
CCAGGTGGAG	TCGACGGCAG	GTTCTGTTGA	GGGCCAGTGG	CGCGGCGCGG	CGGGGACGGC	2640
CGCCCAGGCC	GCGGTGGTGC	GCTTCCAAGA	AGCAGCCAAT	AAGCAGAAGC	AGGAACTCGA	2700
CGAGATCTCG	ACGAATATTC	GTCAGGCCGG	CGTCCAATAC	TCGAGGGCCG	ACGAGGAGCA	2760
GCAGCAGGCC	CTGTCTCTCG	AAATGGGCTT	TGGATTCAGC	TTGCGGCTGC	CTGCTGGCTG	2820
GGTGGAGTCT	GACGCCGCCG	ACTTCGACTA	GGTTTCAGCA	CTCCTCAGCA	AAACCACCGG	2880
GGACCCGCCA	TTTCCCGGAC	AGCCGCCGCC	GGTGGCCAAT	GACACCCGTA	TCGTGCTCGG	2940
CCGGCTAGAC	CAAAAGCTTT	ACGCCAGCGC	CGAAGCCACC	GACTCCAAGG	CCGCGGCCCG	3000
GTTGGGCTCG	GACATGGGTG	AGTTCTATAT	GCCCTACCCG	GGCACCCGGA	TCAACCAGGA	3060
AACCGTCTCG	CTYGACGCCA	ACGGGGTGTC	TGGAAGCGCG	TCGTATTACG	AAGTCAAGTT	3120
CAGCGATCCG	AGTAAGCCGA	ACGGCCAGAT	CTGGACGGGC	GTAATCGGCT	CGCCCGCGGC	3180
GAACGCACCG	GACGCCGGGC	CCCCTCAGCG	CTGGTTTGTC	GTATGGCTCG	GGACCGCCAA	3240
CAACCCGGTG	GACAAGGGCG	CGGCCAAGGC	GCTGGCCGAA	TCGATCCGGC	CTTTGGTTCG	3300
CCCGCCGGCG	GCGCCGGCCG	GGGAAGTCGC	TCCTACCCCG	ACGACACCGA	CACCGCAGCG	3360
GACCTTACCG	GCCTGAGAAT	TCTGCAGATA	TCCATCACAC	TGGCGGCCCG	TCGAGCACCA	3420
CCACCACCAC	CACTGAGATC	CGGCTGCTAA	CAAAGCCCGA	AAGGAAGCTG	AGTTGGCTGC	3480
TGCCACCGCT	GAGCAATAAC	TAGCATAACC	CCTTGGGGCC	TCTAAACGGG	TCTTGAGGGG	3540
TTTTTTGCTG	AAAGGAGGAA	CTATATCCGG	AT			3572

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Val	Gln	Phe	Gln	Ser	Gly	Gly	Asp	Asn	Ser	Pro	Ala	Val	Tyr	Kaa	Xaa
1				5				10						15	
Asp	Gly	Xaa	Arg												
			20												

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Thr	Thr	Val	Pro	Xaa	Val	Thr	Glu	Ala	Arg
1				5				10	

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
1 5 10 15
Xaa Lys

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CTAGTTAGTA CTCAGTCGCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGTGACGA ATTCACTTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CATATGGGCC ATCATCATCA TCATCAGTG ATCGACATCA TCGGGACCAG CCCCACATCC	60
TGGGAACAGG CGGC3GCGGA GGCGGTCCAG CGGGCGCGGG ATAGCGTCGA TGACATCCGC	120
GTGCTCGGG TCATTGAGCA GGACATGGCC GTGGACAGCG CCGGCAAGAT CACCTACCGC	180
ATCAAGCTCG AAGTGTCTT CAAGATGAGG CCGGCGCAAC CGAGGGGCTC GAAACCACCG	240
AGCGGTTCCG CTGAAACGGG CGCCGGCGCC GGTACTGTCTG CGACTACCCC CGCGTCGTCG	300
CCGGTGACGT TGGCGGAGAC CGGTAGCACG CTGCTCTACC CGCTGTTCAA CCTGTGGGGT	360
CCGGCCCTTC ACAGAGAGTA TCCGAACGTC ACGATCACCG CTCAGGGCAC CGGTTCTGGT	420
GCCGGGATCG CGCAGGCCGC CGCCGGGACG GTCAACATTG GGGCCTCCGA CGCCTATCTG	480
TCGGAAGGTG ATATGGCCGC GCACAAGGGG CTGATGAACA TCGCGCTAGC CATCTCCGCT	540
CAGCAGGTCA ACTACAACCT GCCCGGAGTG AGCGAGCACC TCAAGCTGAA CGGAAAAGTC	600
CTGGCGGCCA TGTACCAGGG CACCATCAAA ACCTGGGACG ACCCGCAGAT CGCTGCGCTC	660
AACCCCGGCG TGAACCTGCC CGGCACCGCG GTAGTTCCGC TGCACCGCTC CGACGGGTCC	720
GGTGACACCT TCTTGTTTAC CCAGTACCTG TCCAAGCAAG ATCCCGAGGG CTGGGGCAAG	780
TCGCCCCGCT TCGGCACCAC CGTGCAGTTC CCGGCGGTGC CGGGTGCCTG GGGTGAGAAC	840
GGCAACGGCG GCATGGTGAC CGGTTGCGCC GAGACACCGG GCTGCGTGCC CTATATCGGC	900
ATCAGCTTCC TCGACCAGGC CAGTCAACGG GGAATCGGCG AGGCCCAACT AGGCAATAGC	960
TCTGGAATT TCTTGTTGCC CGACGCGCAA AGCATTCAGG CCGCGGCGGC TGGCTTCGCA	1020
TCGAAAACCC CGGCGAACCA GGCGATTTCT ATGATCGACG GGCCCGCCCC GGACGGCTAC	1080
CCGATCATCA ACTACGAGTA CGCCATCGTC AACAACCGGC AAAAGGACGC CGCCACCGCG	1140
CAGACCTTGC AGGCATTTCT GCACTGGGCG ATCACCAGCG GCAACAAGGC CTCGTTCTCTC	1200
GACCAGGTTT ATTTCCAGCC GCTGCCGCCC GCGGTGGTGA AGTTGTCTGA CGCGTTGATC	1260
GCGACGATTT CCAGCGCTGA GATGAAGACC GATGCCGCTA CCCTCGCGCA GGAGGCAGGT	1320

AATTTTCGAGC GGATCTCCGG CGACCTGAAA ACCCAGATCG ACCAGGTGGA GTCGACGGCA 1380
 GGTTTCGTTGC AGGGCCAGTG GCGCGGCGCG GCGGGGACGG CCGCCCAGGC CGCGGTGGTG 1440
 CGCTTCCAAG AAGCAGCCAA TAAGCAGAAG CAGGAACCTCG ACGAGATCTC GACGAATATT 1500
 CGTCAGGCCG GCGTCCAATA CTCGAGGGCC GACGAGGAGC AGCAGCAGGC GCTGTCTCTG 1560
 CAAATGGGCT TTGTGCCAC AACGGCCGCC TCGCCGCCGT CGACCGCTGC AGCGCCACCC 1620
 GCACCGGCGA CACCTGTTGC CCCCCACCA CCGGCCGCCG CCAACACGCC GAATGCCAG 1680
 CCGGGCGATC CCAACGCAGC ACCTCCGCCG GCGGACCCGA ACGCACCGCC GCCACCTGTC 1740
 ATTGCCCCAA ACGCACCCCA ACCTGTCCGG ATCGACAACC CGGTTGGAGG ATTCAGCTTC 1800
 GCGCTGCCTG CTGGCTGGGT GGAGTCTGAC GCGGCCCACT TCGACTACGG TTCAGCACTC 1860
 CTCAGCAAAA CCACCGGGGA CCGCCATTTC CCGGACAGC CGCCGCCGGT GGCCAATGAC 1920
 ACCCGTATCG TGCTCGGCCG GCTAGACCAA AAGCTTTACG CCAGCGCCGA AGCCACCGAC 1980
 TCCAAGGCCG CGGCCCGGTT GGGCTCGGAC ATGGGTGAGT TCTATATGCC CTACCCGGGC 2040
 ACCCGGATCA ACCAGGAAAC CGTCTCGCTC GACGCCAACG GGGTGTCTGG AAGCGCGTCG 2100
 TATTACGAAG TCAAGTTCAG CGATCCGAGT AAGCCGAACG GCCAGATCTG GACGGGCGTA 2160
 ATCGGCTCGC CCGCGGCGAA CGCACCGGAC GCGGGGCCCC CTCAGCGCTG GTTTGTGGTA 2220
 TGGCTCGGGA CCGCCAACAA CCGGTGGAC AAGGGCGCGG CCAAGGCGCT GGCCGAATCG 2280
 ATCCGGCCTT TGGTCGCCCC GCGCGCGCG CCGGCACCGG CTCCTGCAGA GCGCGCTCCG 2340
 GCGCCGCGCG CGGCCGGGA AGTCGCTCCT ACCCCGACGA CACCGACACC GCAGCGGACC 2400
 TTACCGGCCT GA 2412

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1 5 10 15
 Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
 20 25 30
 Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35 40 45
 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50 55 60
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
 65 70 75 80
 Gly Ser Pro Glu Thr Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
 85 90 95
 Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
 100 105 110
 Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
 115 120 125
 Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
 130 135 140
 Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
 145 150 155 160
 Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
 165 170 175
 Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His

180 185 190
 Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
 195 200 205
 Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
 210 215 220
 Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
 225 230 235 240
 Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
 245 250 255
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
 260 265 270
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
 275 280 285
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp
 290 295 300
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
 305 310 315 320
 Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605
 Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620

Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGATCCAAAC CACCGAGCGG TTCGCCTGAA ACGG

34

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CGCTGCGAAT TCACCTCCGG AGGAAATCGT CGCGATC

37

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

CATATGGGCC ATCATCATCA TCATCACGGA TCCAAACCAC CGAGCGGTTC GCCTGAAACG      60
GGCGCCGGCG CCGGTACTGT CGCGACTACC CCCGCGTCGT CGCCGGTGAC GTTGGCGGAG      120
ACCGGTAGCA CGCTGCTCTA CCCGCTGTTC AACCTGTGGG GTCCGGCCTT TCACGAGAGG      180
TATCCGAACG TCACGATCAC CGCTCAGGGC ACCGGTTCTG GTGCCGGGAT CGCGCAGGCC      240
GCCGCCGGGA CGGTCAACAT TGGGGCCTCC GACGCCTATC TGTCGGAAGG TGATATGGCC      300
GCGCACAAAG GGCTGATGAA CATCGCGCTA GCCATCTCCG CTCAGCAGGT CAACTACAAC      360
CTGCCCCGAG TGAGCGAGCA CCTCAAGCTG AACGGAAAAG TCCTGGCGGC CATGTACCAG      420
GGCACCATCA AAACCTGGGA CGACCCGAG ATCCTGCGC TCAACCCCGG CGTGAACCTG      480
CCCCGCACCG CGGTAGTTCC GCTGCACCGC TCCSACGGGT CCGGTGACAC CTTCTTGTTT      540
ACCCAGTACC TGTCCAAGCA AGATCCCGAG GGCTGGGGCA AGTCGCCCCG CTTCCGSCACC      600
ACCGTCGACT TCCCGGCGGT GCCGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG      660
ACCGGTTGCG CCGAGACACC GGGCTGCGTG GCCTATATCG GCATCAGCTT CCTCGACCAG      720
GCCAGTCAAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTG      780
CCCGACGCGC AAAGCATTCA GGCCGCGGCG GCTGGCTTCG CATCGAAAAC CCCGGCGAAC      840
CAGGCGATTT CGATGATCGA CGGGCCCGCC CCGGACGGCT ACCCGATCAT CAACTACGAG      900
TACGCCATCG TCAACAACCG GCAAAAGGAC GCCGCCACCG CGCAGACCTT GCAGGCATTT      960
CTGCACTGGG CGATCACCGA CGGCAACAAG GCCTCGTTCC TCGACCAGGT TCATTTCCAG     1020
CCGCTGCCGC CCGCGGTGGT GAAGTTGTCT GACGCGTTGA TCGCGACGAT TTCCTCCGGA     1080
GGTGGCAGTG GGGGAGGCTC AGGTGGAGGT TCTGGCGGGA GCGTGCCAC AACGGCCGCC     1140
TCGCCGCCGT CGACCGCTGC AGCGCCACCC GCACCGGCGA CACCTGTTGC CCCCCACCA     1200
CCGGCCGCCG CCAACACGCC JAATGCCAG CCGGGCGATC CCAACGCAGC ACCTCCSCCG     1260
GCCGACCCGA ACGCACCCGC GCCACCTGTC ATTGCCCAA ACGCACCCCA ACCTGTCCCG     1320
ATCGACAACC CGGTTGGAGG ATTCAGCTTC GCGCTGCCTG CTGGCTGGGT GGAGTCTGAC     1380
GCCGCCCACT TCGACTACGG TTCAGCACTC CTCAGCAAAA CCACCGGGGA CCCGCCATTT     1440
CCCGGACAGC CGCCGCCGGT GGCCAATGAC ACCCGTATCG TGCTCGGCCG GCTAGACCAA     1500
AAGCTTTACG CCAGCGCCGA AGCCACCGAC TCCAAGGCCG CGGCCCGGTT GGGCTCGGAC     1560
ATGGGTGAGT TCTATATGCC CTACCCGGGC ACCCGGATCA ACCAGGAAAC CGTCTCGCTC     1620
GACGCCAACG GGGTGTCTGG AAGCGGCTCG TATTACGAAG TCAAGTTCAG CGATCCGAGT     1680
AAGCCGAACG GCCAGATCTG GACGGGCGTA ATCGGCTCGC CCGCGGCGAA CGCACCAGAC     1740
GCCGGGCCCC CTCAGCGCTG GTTTGTGGTA TGCTCGGGA CCGCCAACAA CCCGGTGGAC     1800
AAGGGCGCGG CCAAGGCGCT GGCCGAATCG ATCCGGCCTT TGGTCGCCCC GCCGCCGCGC     1860
CCGGCACCGG CTCCTGCAGA CCCGCTCCG GCGCCGGCGC CGGCCGGGGA AGTCGCTCCT     1920
ACCCCGACGA CACCGACACC GCAGCGGACC TTACCGGCCT GA                               1962

```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Gly His His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1           5           10           15
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20           25           30
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35           40           45
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50           55           60
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 65           70           75           80
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85           90           95
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 100          105          110
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 115          120          125
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 130          135          140
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 145          150          155          160
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 165          170          175
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 180          185          190
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 195          200          205
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 210          215          220
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 225          230          235          240
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 245          250          255
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 260          265          270
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 275          280          285
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 290          295          300
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 305          310          315          320
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 325          330          335
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 340          345          350
Ile Ala Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 355          360          365
Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 370          375          380
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 385          390          395          400
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 405          410          415
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 420          425          430

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Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 435 440 445
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 450 455 460
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 465 470 475 480
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 485 490 495
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 500 505 510
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 515 520 525
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 530 535 540
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 545 550 555 560
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 565 570 575
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 580 585 590
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 595 600 605
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 610 615 620
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 625 630 635 640
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 645 650

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference 9532-023-228	IMPORTANT DECLARATION	Date of mailing (day/month/year) 22 JUNE 1999
International application No. PCT/US99/03265	International filing date (day/month/year) 17 FEBRUARY 1999	(Earliest) Priority Date (day/month/year) 18 FEBRUARY 1998
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant CORIXA CORPORATION		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories.
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practiced on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.

2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
☐ the claims
☐ the drawings

3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:

☒ it does not comply with the prescribed standard
☐ it is not in the prescribed machine readable form

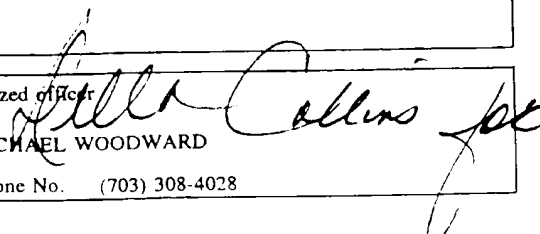
4. Further comments:

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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Form PCT/ISA/203 (July 1992)★

Authorized officer


MICHAEL WOODWARD

Telephone No. (703) 308-4028

**DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT**

International application No.
PCT/US99/03265

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(5): A61K 38/00; C07K 1/00; C07K 16/00; C12Q 1/68; C12P 19/34; C07H 21/02, 21/04
US Cl. 530/300, 350, 387.1; 435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32, 24.33